

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2001, 09:51:08 ; Search time 2146.18 Seconds
(without alignments)
12830.314 Million cell updates/sec

Title: US-09-297-703A-28
Perfect score: 2913
Sequence: 1 ctcttaactctcagcga.....aaaaacaaaaaacatccatg 2913

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 10228115 segs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: gb_est41:*
42: gb_est42:*
43: gb_est43:*

44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_esthum29:*
64: em_esthum30:*
65: em_esthum31:*
66: em_esthum32:*
67: em_esthum33:*
68: em_esthum34:*
69: em_esthum35:*
70: em_esthum36:*
71: em_esthum37:*
72: em_esthum38:*
73: em_esthum39:*
74: em_esthum40:*
75: em_esthum41:*
76: em_esthum42:*
77: em_esthum43:*
78: em_esthum44:*
79: em_esthum45:*
80: em_esthum46:*
81: em_esthum47:*
82: em_esthum48:*
83: em_esthum49:*
84: em_esthum50:*
85: em_esthum51:*
86: em_esthum52:*
87: em_esthum53:*
88: em_esthum54:*
89: em_esthum55:*
90: em_esthum56:*
91: em_esthum57:*
92: em_esthum58:*
93: em_esthum59:*
94: em_esthum60:*
95: em_esthum61:*
96: em_esthum62:*
97: em_esthum63:*
98: em_esthum64:*
99: em_esthum65:*
100: em_esthum66:*
101: em_esthum67:*
102: em_esthum68:*
103: em_esthum69:*
104: em_esthum70:*
105: em_esthum71:*
106: em_esthum72:*
107: em_esthum73:*
108: em_esthum74:*
109: em_esthum75:*
110: em_esthum76:*
111: em_esthum77:*
112: em_esthum78:*
113: em_esthum79:*
114: em_esthum80:*
115: em_esthum81:*
116: em_esthum82:*

117: gb_est48:*
 118: gb_est49:*
 119: gb_est50:*
 120: gb_est51:*
 121: gb_est52:*
 122: gb_est53:*
 123: gb_est54:*
 124: gb_est55:*
 125: gb_est56:*
 126: gb_est57:*
 127: gb_est58:*
 128: gb_est59:*
 129: gb_est60:*
 130: gb_est61:*
 131: gb_est62:*
 132: gb_est63:*
 133: gb_est64:*
 134: gb_est65:*
 135: gb_est66:*
 136: gb_est67:*
 137: gb_est68:*
 138: gb_est69:*
 139: gb_est70:*
 140: gb_est71:*
 141: gb_est72:*
 142: gb_est73:*
 143: gb_est74:*
 144: gb_est75:*
 145: gb_est76:*
 146: gb_est77:*
 147: gb_est78:*
 148: gb_est79:*
 149: gb_est80:*
 150: gb_est81:*
 151: gb_est82:*
 152: gb_est83:*
 153: gb_est84:*
 154: gb_est85:*
 155: gb_est86:*
 156: gb_est87:*
 157: gb_est88:*
 158: gb_est89:*
 159: gb_est90:*
 160: gb_est91:*
 161: gb_est92:*
 162: gb_est93:*
 163: gb_est94:*
 164: gb_est95:*
 165: gb_est96:*
 166: gb_est97:*
 167: gb_est98:*
 168: gb_est99:*
 169: gb_est100:*
 170: gb_est101:*
 171: gb_est102:*
 172: gb_est103:*
 173: gb_est104:*
 174: gb_est105:*
 175: gb_est106:*
 176: gb_est107:*
 177: gb_est108:*
 178: gb_est109:*

190: gb_est110:*
 191: gb_est111:*
 192: gb_hic:*
 193: em_gss_fun:*
 194: em_gss_hum1:*
 195: em_gss_hum2:*
 196: em_gss_hum3:*
 197: em_gss_hum4:*
 198: em_gss_hum5:*
 199: em_gss_hum6:*
 200: em_gss_hum7:*
 201: em_gss_hum8:*
 202: em_gss_hum9:*
 203: em_gss_inv1:*
 204: em_gss_inv2:*
 205: em_gss_inv3:*
 206: em_gss_other:*
 207: em_gss_pln1:*
 208: em_gss_pln2:*
 209: em_gss_pro:*
 210: em_gss_rod1:*
 211: em_gss_rod2:*
 212: em_gss_rod3:*
 213: em_gss_rod4:*
 214: em_gss_rod5:*
 215: em_gss_vrt1:*
 216: em_gss_vrt2:*
 217: em_gss_vrt3:*
 218: gb_gss1:*
 219: gb_gss2:*
 220: gb_gss3:*
 221: gb_gss4:*
 222: gb_gss5:*
 223: gb_gss6:*
 224: gb_gss7:*
 225: gb_gss8:*
 226: gb_gss9:*
 227: gb_gss10:*
 228: gb_gss11:*
 229: gb_gss12:*
 230: gb_gss13:*
 231: gb_gss14:*
 232: gb_gss15:*
 233: gb_gss16:*
 234: gb_gss17:*
 235: gb_gss18:*
 236: gb_gss19:*
 237: gb_gss20:*
 238: gb_gss21:*
 239: gb_gss22:*
 240: gb_gss23:*
 241: gb_gss24:*
 242: gb_gss25:*
 243: gb_gss26:*
 244: gb_gss27:*
 245: gb_gss28:*
 246: gb_gss29:*
 247: gb_gss30:*
 248: gb_gss31:*
 249: gb_gss32:*
 250: gb_gss33:*
 251: gb_gss34:*
 252: em_gss_inv4:*
 253: em_gss_rod6:*
 254: em_gss_rod7:*
 255: em_gss_rod8:*
 256: gb_gss35:*
 257: gb_gss36:*
 258: gb_gss37:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

REFERENCE

JOURNAL AUTHORS	2 (sites) Methods Enzymol. 303, 19-44 (1999)
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL MEDLINE REFERENCE AUTHORS	Genome Res. 10 (10), 1617-1630 (2000) 20493374 3 (sites) Shibata, K., Itoh, M., Alizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakeguchi, S., Ikegami, T., Hashidagui, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M., Yoneeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipipillary sequencer
TITLE	Genome Res. 10 (11), 1757-1771 (2000) 20530913 4 (sites) The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium
JOURNAL MEDLINE REFERENCE AUTHORS	Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 (bases 1 to 2738) Adachi, J., Alizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Araiawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hayasagi, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, D., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Soabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, T.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-test@ssc.riken.go.jp, URL: http://genome. gsc.riken. go. jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	Please visit our web site (http://genome. gsc.riken. go. jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in RIKEN

Submitted (v-001-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9216, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAAGAGAGACGATTCAGGAGGACGCTCTTTTCTTTTTCVN 3'], cDNA was prepared by using Trnascribe thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAAGAGAGACTTCGAGTTAATTAATTAATCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: *SOB*.

Location/Qualifiers

KEYWORDS	SOURCE
CAP trapper	1..2738
Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,	/organism="Mus musculus"
clone.lib=RKEN full-length enriched mouse cDNA library	/strain="C57BL/6J"
clone:2310045H19.	/db_xref="taxon:10090"
	/db_xref="MCD:MGI:1907315"
	/db_xref="MCD:MGI:1921435"
	/clone="2310045H19"
	/sex="male"
	/tissue_type="tongue"
	/clone.lib="RKEN full-length enriched mouse cDNA library"
	/dev_stage="adult"

CDS
21.. 2129
/note="putative"
/codon_start=1
/protein_id="BAB26519.1"
/ID_xref="GI:12844842"
/translation="MAAPAPAGTGGPDARLEALADYPELARLEIDPYKFPAD
FORRYKFSQVLDIGENEGIDKFSKESFGRHSDGGLYCKEMAPGEGPLIG
EFGMNPFSHPYKLELYGKWEYIPKONKSPILPHGSKLAVITKSGELLINISW
AKYVRENUNNVNDIMHAPEDPYKFKHSRPPKSLIYSHVGISHEKLIASVK
FTSNVLPRIKDLGYNCTIOLMAIMEHAYVASFQYITSEFSAASRYGPEELKEVDA
HSGNIVLIDVYHSHASKNSKSDGDMFDSCTPHSGPGRHDLMSRLFTYSMEV
LRLSLNIRKMLEEYCFDFGRDQVSMYHHRMGOGSGDYNFELOYDEDLITY
KIDDMNGNIVYTLITNRYLEKCAVAFSDALVGDGKFLAWLADALMTNMSLAP
FTPVIDRGIOLHRIKILITHIGEGYINPMNGENEGHPWLDOPRKNESYHVARO
FNLLDDLLKFKFLNNDRDMLNERCGLSAPQAYVEKHEANKITFERAGLLFI
FNHPKSYTDYRVGTATPGKFIYVDSDAAYEGHQRDLHNTNYFAFAFEHNGRPS
LYVIPSRAVLIQNDLON"

polyA_signal
2714..2719
/note="putative"
2738
polyA_site
/note="putative"
BASE COUNT 780 a 562 c 624 g 772 t
ORIGIN

Query Match 19.7% Score 573, DB 192, Length 2738:
Best Local Similarity 57.2% Pred. No. 2,7e-149;
Matches 1166; Conservative 0; Mismatches 825; Indels 48; Gaps 5;

463 gacatagatccaagctttacaggtttcgtcaaacactagattacggtattccacagtac 521
DB 117 GAGATTGACCGGTACTACAGCCCTTCGCCCGGACATTCCAGCCAGGTATAGAAATT 176
117 GAGATTGACCGGTACTACAGCCCTTCGCCCGGACATTCCAGCCAGGTATAGAAATT 176
522 aaaaagctccgagaagaattgacaagatagaagtagtgcgtgtagtcaattctcgtgac 581
DB 177 ACCCAGGTTTTCATGACATTGGAGAGAAATGAGTGGATGATAGTTCTCCAGAGGC 236
177 ACCCAGGTTTTCATGACATTGGAGAGAAATGAGTGGATGATAGTTCTCCAGAGGC 236
582 tatgaaaagtttggtt---ctcagcagtgtaaacaggaataacttatagagtgagga 638
DB 237 TATGAGTCTATTGGCATCCACAGATGTTCTATGGTGGCATCTACGCAAGATGGGCC 296
237 TATGAGTCTATTGGCATCCACAGATGTTCTATGGTGGCATCTACGCAAGATGGGCC 296
639 ccaagagtaagtgagtgagtgatgagattgaaataacttaacttaagagtgagga 698
DB 297 CCAAGAGCAAGAGGAGTTTCTTACTGAGAAATTCAGTGGTGGAAATCCATTTCTCAC 356
297 CCAAGAGCAAGAGGAGTTTCTTACTGAGAAATTCAGTGGTGGAAATCCATTTCTCAC 356
699 gtcatactcagaatgagtgagtgctcgtgagagatccttttgcggaataatgacagtg 758
DB 357 CCATATATAAAAGCTGGAATACGAAATAAGGAGCTGTATATCCACCCACAGACAAA 416
357 CCATATATAAAAGCTGGAATACGAAATAAGGAGCTGTATATCCACCCACAGACAAA 416
759 tcaaccaaatccccaatggtctcgtagtaagatacagcatgatactcaactcgtgcaac 818
DB 417 TCCCCCTGATACCTCATGCGTCAAGCTGAAGGTAATTACTAGTAAGAGTGGCAG 476
417 TCCCCCTGATACCTCATGCGTCAAGCTGAAGGTAATTACTAGTAAGAGTGGCAG 476
819 aaa---gattcattccttgctgtaucaagtgctcaagtgcaagcaacagtgaaactcca 875
DB 477 ATTCGTGTATCGGATTTCCCATGAGCAAAAGTATGTGTTCCGAGAACACAACTGAC 536
477 ATTCGTGTATCGGATTTCCCATGAGCAAAAGTATGTGTTCCGAGAACACAACTGAC 536
876 tataatgcatatactatgatactcctccgagagagagagatgtagttaaataacctcag 935
DB 537 TATGATTGGATACACTGGGCTCC---AGAGACCCCTATATAAATTAAGACATCCAGA 590
537 TATGATTGGATACACTGGGCTCC---AGAGACCCCTATATAAATTAAGACATCCAGA 590
936 ccaagaagacccaataactcactcgtgatttagtcgacgcttgatagtagttagcagag 995
DB 591 CCAAGAGCAAGAGGAGCTTAAGAAATTTGAAATCTCATGTGGAAATTTCTCCACAGAA 650
591 CCAAGAGCAAGAGGAGCTTAAGAAATTTGAAATCTCATGTGGAAATTTCTCCACAGAA 650
996 ccagtaattacaacatactgccaactttagagatgagtggtctcctcgcataaaaagctt 1055
DB 651 GGAATAATACCTCTTACAAACATTTTACACCAATGTACTACCAAGATCAAAACACTT 710
651 GGAATAATACCTCTTACAAACATTTTACACCAATGTACTACCAAGATCAAAACACTT 710
1056 ggtctacaagtgcttcaagctcagctatcgaagcattcatatagctattgagcttgg 1115
DB 711 GGGTATATACTGATCAGTTGATGCGCATCAGAACATGCTTACTATGCCAGTTTGGG 770
711 GGGTATATACTGATCAGTTGATGCGCATCAGAACATGCTTACTATGCCAGTTTGGG 770

1116 tacaagtcacaacttttatgagctagcagcgagtttggaaactcctgatattaaag 1175
DB 771 TACCAATCGACGAGCTTTTTCGACCTTCAGCTGATATGAGAACTCTCGAAGAGCTGAAA 830
771 TACCAATCGACGAGCTTTTTCGACCTTCAGCTGATATGAGAACTCTCGAAGAGCTGAAA 830
1176 tcttaataagataaagctcaagagtaggtctctctgtcttcaatgataattgttcaagc 1235
DB 831 GAACCTTTGACACACACACATTGATGGGCAATGTATGCTCTCTAGATGTGTTGATAGC 890
831 GAACCTTTGACACACACACATTGATGGGCAATGTATGCTCTCTAGATGTGTTGATAGC 890
1236 catgcatcaactaatacgtttagtgagtcgataatgattgtagtgagtagtgtaaac 1295
DB 891 CATCTTCAAAAATTCAGAAATGGGTTAAACATGTTGATGGGACCGATTCCTGTTAT 950
891 CATCTTCAAAAATTCAGAAATGGGTTAAACATGTTGATGGGACCGATTCCTGTTAT 950
1296 tttaaccttgagacacaggggtcaatcttagtgagtcgactcgcctttcaacataggg 1355
DB 1011 AGCTGGAGAGTTTAAAGATCTTCTGTCGAAACATTAAGATGGTGGAGAGTACTGC 1070
1011 AGCTGGAGAGTTTAAAGATCTTCTGTCGAAACATTAAGATGGTGGAGAGTACTGC 1070
1416 tttagtggttgcagatttgatgggtgagcttcaatgataccatcatgattgcag 1475
DB 1071 TTTGATGGCTTCGTTTGTATGGTGTCACCTCTATCATCATCCACGGAATGGGT 1130
1071 TTTGATGGCTTCGTTTGTATGGTGTCACCTCTATCATCATCCACGGAATGGGT 1130
1476 gtagatttaccgcaactcaatgaatacttgaatatgacaatgataatgataatg 1535
DB 1131 CAAGTTTTCGGGTGACCTAATGAATATTTTGGACTACAACTAGATGAATGATGCTTGG 1190
1131 CAAGTTTTCGGGTGACCTAATGAATATTTTGGACTACAACTAGATGAATGATGCTTGG 1190
1536 gtttaatttgatgctgttgatgataatgataatgataatgataatgataatgataat 1595
DB 1191 ATTATCTCATAGTTGGCAAAATTCATGTTGGCTGATCCCACTGATGATGATGATGAT 1250
1191 ATTATCTCATAGTTGGCAAAATTCATGTTGGCTGATCCCACTGATGATGATGATGAT 1250
1596 gttgagatgcttagtgatgagtgacacagtgatgacatccggttgaagatggtgtg 1655
DB 1251 GCAGAGATGATATCAGAGATCCCGCTCTCTGTTCTCCAACTTCCAGGAGGCGGTGCT 1310
1251 GCAGAGATGATATCAGAGATCCCGCTCTCTGTTCTCCAACTTCCAGGAGGCGGTGCT 1310
1656 ttgattatcgtctccacatgagtgctgtcgtgataaattggttgaagattatcgaag 1712
DB 1311 TTTGACATCAATTAAGCAATGCTATTCAGATGAAATGATGATGATGATGATGATGAT 1370
1311 TTTGACATCAATTAAGCAATGCTATTCAGATGAAATGATGATGATGATGATGATGAT 1370
1713 agagatgagagttgaaatgagtgagatgataatgataatgataatgataatgataat 1772
DB 1371 AAAGATGAGAGCTGAATATGGAATATGATGATGATGATGATGATGATGATGATGAT 1430
1371 AAAGATGAGAGCTGAATATGGAATATGATGATGATGATGATGATGATGATGATGAT 1430
1773 gaaagtgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1832
DB 1431 GAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1490
1431 GAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1490
1833 gcaatttgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1892
DB 1491 GCGTTTGGTGTGATGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1550
1491 GCGTTTGGTGTGATGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1550
1893 ccttcataagatcgttgagatgagatgagatgagatgagatgagatgagatgagatgag 1952
DB 1551 CCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1610
1551 CCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1610
1953 ggcgagagaagatattgaattttagtgagaaatgagaaatgagaaatgagaaatgagaa 2012
DB 1611 GGTGAGAGAGCTATCAATTTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1670
1611 GGTGAGAGAGCTATCAATTTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1670
2013 ttccaagagtgatcctatcctccagtggttaatttgccttgagaaacttaacag 2072
DB 1671 TTCCCAAGGAAA-----GGAATATGAGAGT 1697
1671 TTCCCAAGGAAA-----GGAATATGAGAGT 1697
2073 tatgataaagtcgagcgttagtgatttagcgaatcaaaagcatcagagatcaatgag 2132
DB 1698 TACCATTTAGCGAAGAGAGGATTAATTAAACGAGATGACCTTCTCGATATAAGTTC 1757
1698 TACCATTTAGCGAAGAGAGGATTAATTAAACGAGATGACCTTCTCGATATAAGTTC 1757
2133 atgcaagatlttgatcaagcaatcagcaatccttgagaagaagcattgattcaactct 2192
DB 1758 CTAATATACCTTGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1817
1758 CTAATATACCTTGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1817

QY 2193 gaggccaatacatatcaccggaagatgaagatgcgatactgtcttcgagaggga 2252
 Db 1818 CCACGAGCCCTGAGTGAAGAAACATGAAGCAATACCTTTGAGAGACA 1877
 QY 2253 aacctggttttgtatcaatttccttgactagcagctatcgattaccaggttgc 2312
 Db 1878 GGACTTCTCTTATTTTCAACTTCCACGACGACGATATACGACATCCGAGTCGGG 1937
 QY 2313 tgcataagcgaagaaatgaagaatgccttgactatgaatgccttctgttgagagc 2372
 Db 1938 ACAGCAACACGACGAGAAATTTACTAGATTCTGACGACGAGATATGAGAGT 1997
 QY 2373 ttgtgacaggttagatcatgacagacacttgcagcttgagaggtgtgacataaccg 2432
 Db 1998 CATCAAGAGACTGACCAACACCACTACTGTTGAGGCTTTGACATATATGGGCC 2057
 QY 2433 cctcgatccttcattgtgtacacacacatgtagacagcagtggtctatgttgaga 2491
 Db 2058 CCTATTCTCTTCTGTTGATCAATCCAGCCGAGTGGCTCATCTTCAGATGTGA 2116

RESULT 2
 BE602527 731 bp mRNA EST 02-MAR-2001
 LOCUS BE602527
 DEFINITION HVSMH009922f Hordeum vulgare 5-45 DAP spike EST library
 HVCNMA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMH009922f,
 mRNA sequence.
 BE602527
 VERSION BE602527.2 GI:13190371
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 ; Triticeae; Hordeum.
 1 (bases 1 to 731)
 Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu
 ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
 ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
 Wood,T.
 Development of a genetically and physically anchored EST resource
 for barley genomics
 Unpublished (2000)
 JOURNAL On Aug 21, 2000 this sequence version replaced gi:9860088.
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: AATTACCCCTCACTAAGG
 High quality sequence stop: 679.
 FEATURES
 source
 1..731
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMH009922f"
 /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
 HVCNMA0009 (5 to 45 DAP)"
 /tissue_type="5-45 DAP spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 194 a 132 c 186 g 216 t 3 others
 ORIGIN

Query Match 15.5%; Score 452.4; DB 137; Length 731;
 Best Local Similarity 77.2%; Pred. NO. 1.2e-115;
 Matches 561; Conservative 0; Mismatches 164; Indels 2; Gaps 1;
 QY 1295 cttcaactgtgacacgggtcatcatgtgtgactctgcctttcaactatg 1354

|||||
 Db 7 CTTTCATGGCGCTCACGGGCACTGATGGGATTCCTGTTCACTACGCG 66
 QY 1355 gactgggaaggttctaaggttcttcttcaatgaagatggtgtgtgatagtacaa 1414
 Db 67 GAATGAAGAAAGTTAAAGGTTTACTTTCCAAATGCCAGATGGGGCTTAGAATATA 126
 QY 1415 gtttgatggttgatgttgatgttggtgactgaatgatgaacccatattgtga 1474
 Db 127 GTTTCATGGGTTCCCATTCGACGGGCCCATCTCATATGATATCCCATGATATCA 186
 QY 1475 ggtatatttaccgcaactcaatgaatgaatgaatgaatgaatgaatgaatgaatga 1534
 Db 187 AGTACCTTT-ACAGGACTACATGATATTTTGGCTTTCCCGAGATGATGAGT 244
 QY 1535 ggttattatgtcgtgtgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1594
 Db 245 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
 QY 1595 tgtgaagaatgtgtgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1654
 Db 305 TGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 364
 QY 1655 ctgtatattatgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1714
 Db 365 TTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
 QY 1715 agatgaagaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1774
 Db 425 CGATCAAGGTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
 QY 1775 aaagtgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1834
 Db 485 AAAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 544
 QY 1835 atttgctgtatgacaaagatgatgatgatgatgatgatgatgatgatgatgatgat 1894
 Db 545 ATTGCGTGTATGACAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 604
 QY 1895 tctcatagatcgtgtgagtagcatgacaaatgaatgaatgaatgaatgaatgaatga 1954
 Db 605 TAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
 QY 1955 cgggaagaagatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 2014
 Db 665 AGGAGAGGTTATCTTATCTTATGGAATGATGATGATGATGATGATGATGATGAT 724
 QY 2015 tccaaga 2021
 Db 725 TCCAAGA 731

RESULT 3
 BE195628 801 bp mRNA EST 02-MAR-2001
 LOCUS BE195628
 DEFINITION HVSMH008920f Hordeum vulgare 5-45 DAP spike EST library
 HVCNMA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMH008920f,
 mRNA sequence.
 BE195628
 VERSION BE195628.2 GI:13188305
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 ; Triticeae; Hordeum.
 1 (bases 1 to 801)
 Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu
 ,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
 ,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
 Wood,T.
 Development of a genetically and physically anchored EST resource
 for barley genomics

[illegible]

```

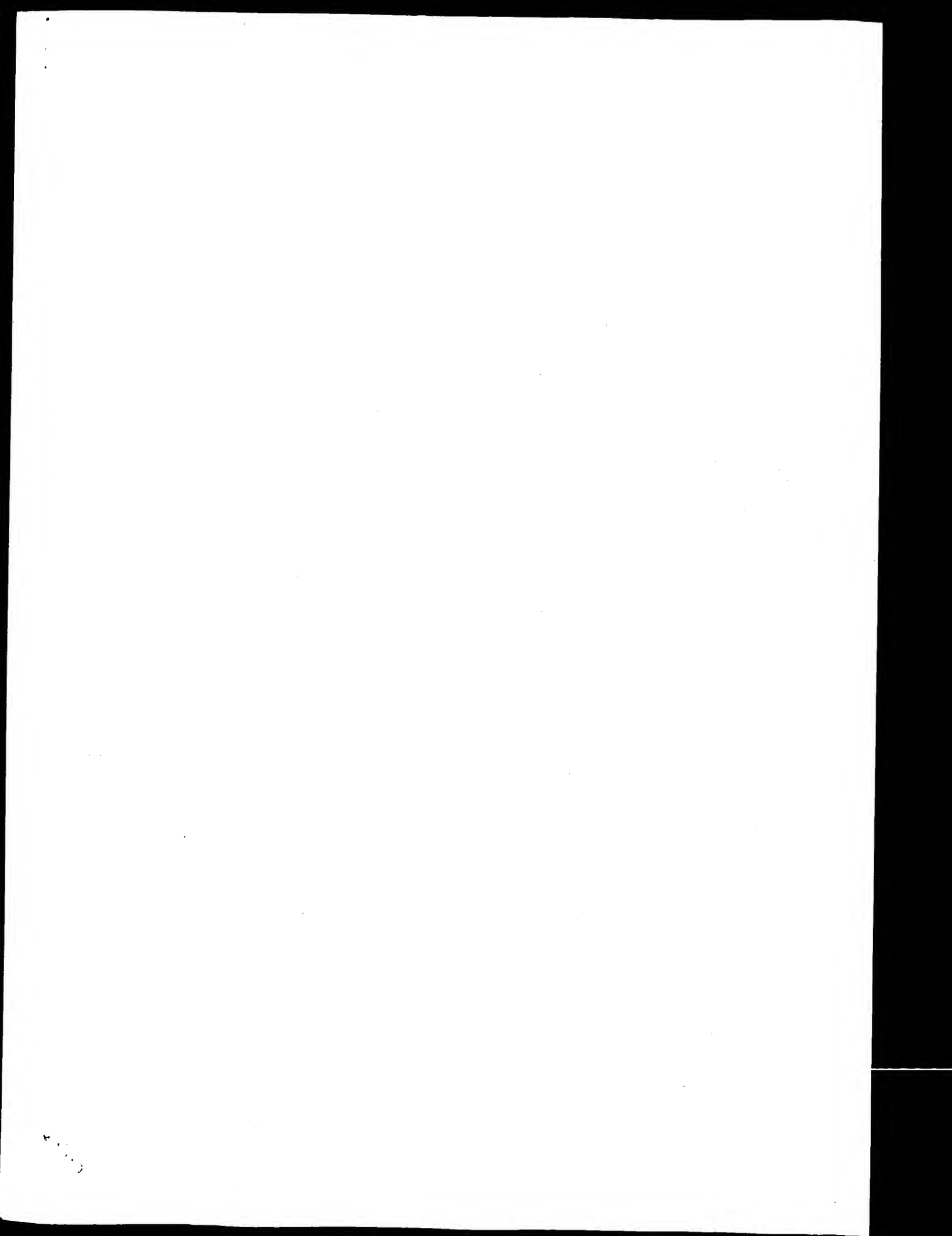
FEATURES
SOURCE
    Location/Qualifiers
      1..565
        /organism="Zea mays"
        /cultivar="Ohio43"
        /db_xref="taxon:4577"
        /clone_id="605"
        /tissue_type="nucellar, embryo, and endosperm"
        /dev_stage="10-14 days post-pollination"
        /lab_host="DH5(alpha)"
        /note="Organ: kernel; Vector: pAD-GAL4-2; Site_1: EcoRI; Site_2: XhoI; Kernel endosperm cDNA library from schmidt lab"
BASE COUNT
161 a 103 c 140 g 160 t 1 others
ORIGIN

```


Fri Aug 10 16:32:42 2001

us-09-297-703a-28.Aug9.rst

Page 15



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2001, 11:02:38 ; Search time 184.84 Seconds
(without alignments)
9895.463 Million cell updates/sec

Title: US-09-297-703a-28

Perfect score: 2913
Sequence: 1 cctctactctcagcgaa.....aaaacaaaaaatccatg 2913

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N.Geneseq_0601.*
2: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/NA1990.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/NA1991.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.*
23: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2913	100.0	2913	19 AAV38719	Full length cassava
2	2028	69.6	3090	19 AAV38720	Full length cassava
3	1384	47.5	3074	18 AAT69587	Potato starch bran
4	1381.2	47.4	2578	17 AAT42631	Class A starch bra
5	1378.4	47.3	2531	17 AAT17267	Class A starch bra
6	1377.8	47.3	3231	17 AAT42632	Class A starch bra
7	1376.8	47.3	2529	17 AAT42637	Class A starch bra
8	1371.4	47.1	2715	21 AAT42639	Arabidopsis thalia
9	1367.2	46.9	2576	17 AAT42636	Class A starch bra
10	1364	46.8	3033	17 AAT42630	Class A starch bra
11	1357.8	46.6	3003	17 AAT42634	Class A starch bra

12	1341.2	46.0	2975	17 AAT42635	Class A starch bra
13	1298	44.6	2919	15 AAO73750	Rice starch branch
14	1292.6	44.4	3015	19 AAV05639	Rice type IV starch
15	1256.6	43.1	2640	19 AAV70961	DNA encoding maize
16	1251.8	43.0	2665	18 AAT69729	Plasmid pBE240 Ins
17	1251.8	43.0	2725	19 AAV29757	Zea mays starch br
18	1194.8	41.0	2725	19 AAV38722	DNA encoding star
19	1098.4	37.7	2307	21 AAZ99938	DNA encoding part
20	1097	37.7	2087	18 AAT69737	Corn starch branch
21	1095.4	37.6	2165	18 AAT69736	Corn starch branch
22	1062.6	36.5	1069	19 AAV38721	Corn starch branch
23	789.4	27.1	1452	21 AAC36957	Arabidopsis thalia
24	633.4	21.7	2487	21 AAT69747	Corn starch branch
25	633.4	21.7	2565	18 AAT69752	Corn starch branch
26	633.4	21.7	2763	19 AAT29758	Zea mays starch br
27	633.4	21.7	2771	13 AAO24257	Branching enzyme D
28	633.4	21.7	2772	18 AAT69740	Plasmid pBE5 Inse
29	627	21.5	2733	15 AAO62135	Rice starch branch
30	625.2	21.5	2687	20 AAX34664	WSE I-D4 cDNA seq
31	623.8	21.4	2733	15 AAO62135	Potato starch bran
32	605.2	20.8	3128	16 AAT00774	DNA encoding maize
33	592.4	20.3	2713	19 AAV70962	Potato amylose-amy
34	587.8	20.2	2909	13 AAO27778	Corn starch branch
35	546.8	18.8	1809	18 AAT69753	Corn starch branch
36	546.8	18.8	1865	18 AAT69748	Maize starch branch
37	384.8	13.2	8119	21 AAZ35392	Nucleotide sequenc
38	376.8	12.9	977	21 AAZ29947	Rice starch branch
39	376.8	12.9	12151	15 AAO62137	Consensus sequence
40	376.2	12.9	1085	21 AAZ39962	Nucleotide sequenc
41	373.6	12.8	979	21 AAZ39962	Rice starch branch
42	373.6	12.8	12151	15 AAO54676	Nucleotide sequenc
43	370.4	12.7	984	21 AAZ29946	Potato starch bran
44	369	12.7	11475	19 AAV54979	Full length potat
45	369	12.7	11478	18 AAT79784	

ALIGNMENTS

AAV38719	1	AAV38719 standard; cDNA; 2913 BP.
ID	AAV38719	standard; cDNA; 2913 BP.
AC	AAV38719;	
XX	XX	
DT	21-SEP-1998	(first entry)
XX	XX	
DE	Full length cassava tuber cDNA in pSJ107.	
XX	XX	
KW	Starch branching enzyme; SBE; cassava; ss.	
XX	XX	
OS	Manihot esculenta.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	21..2531
FT		/*tag= a
FT		/product= SBE II
XX	XX	
PN	WO9820145-A2.	
XX	XX	
PD	14-MAY-1998.	
XX	XX	
PF	04-NOV-1997;	97MO-GB03032.
XX	XX	
PR	05-NOV-1996;	96GB-0023095.
XX	XX	
PA	(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.	
XX	XX	
PI	Jobling SA, Safford R;	
XX	XX	
DR	WPI: 1998-286958/25.	
XX	XX	
DR	P-PSDB; AAM62599.	
XX	XX	

Class A starch bra
Rice starch branch
Rice type IV starch
DNA encoding maize
Plasmid pBE240 Ins
Zea mays starch br
DNA encoding star
DNA encoding part
Corn starch branch
Corn starch branch
Corn starch branch
Arabidopsis thalia
Corn starch branch
Zea mays starch br
Branching enzyme D
Plasmid pBE5 Inse
Rice starch branch
WSE I-D4 cDNA seq
Potato starch bran
DNA encoding maize
Potato amylose-amy
Corn starch branch
Corn starch branch
Maize starch branch
Nucleotide sequenc
Rice starch branch
Consensus sequence
Nucleotide sequenc
Rice starch branch
Nucleotide sequenc
Potato starch bran
Full length potat

PF Starch branching gene from cassava - useful for producing altered
 PT plants giving modified starch
 XX
 XX Claim 2: Fig 4: 67bp; English.
 CC The present sequence encodes starch branching enzyme (SBE) II. It
 CC was isolated from cassava tubers. The products can be used for
 CC producing plants having altered starch quantities and qualities.
 CC They can also be used for producing altered plants such as cassava,
 CC banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
 CC and rice plants.
 XX
 XX Sequence 2913 BP; 818 A; 549 C; 680 G; 866 T; 0 other:

Query Match 100.0%; Score 2913; DB 19; Length 2913;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2913; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctctcctaactctcagagaatgggaactacacacatacagaatacgtttctctgtg 60
 DB 1 ctctcctaactctcagagaatgggaactacacacatacagaatacgtttctctgtg 60
 QY 61 ctccactctgcaaatctcaatctaccggtctccatggtatcgcgagagaccctctgtgc 120
 DB 61 ctccactctgcaaatctcaatctaccggtctccatggtatcgcgagagaccctctgtgc 120
 QY 121 ttctctcaacttcaagagagcgtttcttagagaggtctctctcggaagatcgtatg 180
 DB 121 ttctctcaacttcaagagagcgtttcttagagaggtctctctcggaagatcgtatg 180
 QY 181 aatctgactccctcaaatatgaatgctactgctctcaaaaaggtctctccgagatgctga 240
 DB 181 aatctgactccctcaaatatgaatgctactgctctcaaaaaggtctctccgagatgctga 240
 QY 241 ttgaatgctatctctctcacaacagatcaattggaaagccctggagacggtttcgaagaat 300
 DB 241 ttgaatgctatctctctcacaacagatcaattggaaagccctggagacggtttcgaagaat 300
 QY 301 cccaaggtctctactgacttgaaggtctcattatgagatgagatattgttgaagaatgaa 360
 DB 301 cccaaggtctctactgacttgaaggtctcattatgagatgagatattgttgaagaatgaa 360
 QY 361 taaataaagaatctgttccaaatgagagagacgtttaacatcagaanaaattgataaac 420
 DB 361 taaataaagaatctgttccaaatgagagagacgtttaacatcagaanaaattgataaac 420
 QY 421 caaggtcattctctccaccgagagagaggaagaatataatgacatagatccaaagcttga 480
 DB 421 caaggtcattctctccaccgagagagaggaagaatataatgacatagatccaaagcttga 480
 QY 481 caaggtcttctcaaacactagattacgggtattcacaagtacaanaaagactccagaagaa 540
 DB 481 caaggtcttctcaaacactagattacgggtattcacaagtacaanaaagactccagaagaa 540
 QY 541 ttgacaagtatgaagtagtctgagatgacattctctgtggtcattgaaaagttgtttct 600
 DB 541 ttgacaagtatgaagtagtctgagatgacattctctgtggtcattgaaaagttgtttct 600
 QY 601 caagcagtgaaacaggaataacttataagagatgagagacagagacgttaagtgtggtcat 660
 DB 601 caagcagtgaaacaggaataacttataagagatgagagacagagacgttaagtgtggtcat 660
 QY 661 tgaattgagaatttcaataactgaaatcctaataatgacagtgtcaatgactaagaatgagtg 720
 DB 661 tgaattgagaatttcaataactgaaatcctaataatgacagtgtcaatgactaagaatgagtg 720
 QY 721 gtgtctcgagagatcttcttgcggaataatgagatggttccacacaaatccccaatggtt 780
 DB 721 gtgtctcgagagatcttcttgcggaataatgagatggttccacacaaatccccaatggtt 780
 QY 781 ctggaataagaatagcagatgactccactcggcaaaaagaattctattctctgttga 840
 DB 781 ctggaataagaatagcagatgactccactcggcaaaaagaattctattctctgttga 840

DB 781 ctggaataagaatagcagatgactccactcggcaaaaagaattctattctctgttga 840
 QY 841 tcaagttcagttcagaacacagagtgaaactcccaataatgagcattactcagatcctc 900
 DB 841 tcaagttcagttcagaacacagagtgaaactcccaataatgagcattactcagatcctc 900
 QY 901 ccgagagagagagatgtgttcaaaaatccctcagacgaagaagacaaatcctcttga 960
 DB 901 ccgagagagagagatgtgttcaaaaatccctcagacgaagaagacaaatcctcttga 960
 QY 961 ttatagtcgcacgtttggaatgagtagtagagagccagtgattataacacataatgcact 1020
 DB 961 ttatagtcgcacgtttggaatgagtagtagagagccagtgattataacacataatgcact 1020
 QY 1021 ttgagatagtggtctctccagacacaaagcttgctacaaatgctgttccactcagtg 1080
 DB 1021 ttgagatagtggtctctccagacacaaagcttgctacaaatgctgttccactcagtg 1080
 QY 1081 ctattcaagagacattcattatgctagcttgggtatcacgttacaactttatgcag 1140
 DB 1081 ctattcaagagacattcattatgctagcttgggtatcacgttacaactttatgcag 1140
 QY 1141 ctgaagacagcagattggaaacccctgataagattaaagctcttaataagataaagctcaagat 1200
 DB 1141 ctgaagacagcagattggaaacccctgataagattaaagctcttaataagataaagctcaagat 1200
 QY 1201 taggtctctctgttccatgagatatgtttcataagcactgacataactaactttagatg 1260
 DB 1201 taggtctctctgttccatgagatatgtttcataagcactgacataactaactttagatg 1260
 QY 1261 ggcctgaataatgttgaatgtagtcagatgtgcactactctcctctggaacccaggggtcactc 1320
 DB 1261 ggcctgaataatgttgaatgtagtcagatgtgcactactctcctctggaacccaggggtcactc 1320
 QY 1321 attgagatgtaggactcccgctcttcaactatgtagagcttgagaggttccaaagttctctc 1380
 DB 1321 attgagatgtaggactcccgctcttcaactatgtagagcttgagaggttccaaagttctctc 1380
 QY 1381 ttcaaaaagcagaagtggtgttggatgagatgagacaggtttatgaggttccaaatgaggg 1440
 DB 1381 ttcaaaaagcagaagtggtgttggatgagatgagacaggtttatgaggttccaaatgaggg 1440
 QY 1441 tgaactcaatgagtatacccatcattgagattgagatgagattttacccgcaacacaaatg 1500
 DB 1441 tgaactcaatgagtatacccatcattgagattgagatgagattttacccgcaacacaaatg 1500
 QY 1501 aatacttggatagtagcagactgagatgagatgagatgagatgagatgagatgagatgagatg 1560
 DB 1501 aatacttggatagtagcagactgagatgagatgagatgagatgagatgagatgagatgagatg 1560
 QY 1561 tgaattcagtgctctccacagagagcgttcaacaaattggtgaagaatgtagtgaatgagaa 1620
 DB 1561 tgaattcagtgctctccacagagagcgttcaacaaattggtgaagaatgtagtgaatgagaa 1620
 QY 1621 caatttgcattctccgtttgagaatgagatgagatgagatgagatgagatgagatgagatgagatg 1680
 DB 1621 caatttgcattctccgtttgagaatgagatgagatgagatgagatgagatgagatgagatgagatg 1680
 QY 1681 tctcgtgataaagtggtgttgaatattcagaagaagagatgagaatgagaatgagaatgagaatgaga 1740
 DB 1681 tctcgtgataaagtggtgttgaatattcagaagaagagatgagaatgagaatgagaatgagaatgaga 1740
 QY 1741 ttgtacataatgctgacaacaaagcggtgttgaagaatggttctctatactgtaaaagtc 1800
 DB 1741 ttgtacataatgctgacaacaaagcggtgttgaagaatggttctctatactgtaaaagtc 1800
 QY 1801 atgacaagagcctctgttggagacaacaaatgagatttggctgagatgagaagaatgagatgagatgag 1860
 DB 1801 atgacaagagcctctgttggagacaacaaatgagatttggctgagatgagaagaatgagatgagatgag 1860
 QY 1861 atgagacttcaatgagcttcttgaagacacatactactcctcactcactgagatgagatgagatgag 1920
 DB 1861 atgagacttcaatgagcttcttgaagacacatactactcctcactcactgagatgagatgagatgagatgag 1920

QY	1921	acnaatggtcagcgcttattacaatggggaatttagggcggaagagatatttgaatttagg	1980
Dp	1921	acanaaaagacaaagccttattaccaatgggctctatggcggaagagatatttgaatttagg	1980
QY	1981	gaatgattctggacaccccgagctgattgatttctccaaagagtgatcatctccca	2040
Dp	1981	gaatgattctggacaccccgagctgattgatttctccaaagagtgatcatctccca	2040
QY	2041	gtcgtaaatgttctctgggaacaattaaagttatgataaattgcgcgggtaggttgatc	2100
Dp	2041	gtcgtaaatgttctctgggaacaattaaagttatgataaattgcgcgggtaggttgatc	2100
QY	2101	taggaacttcaaaagcactctgagatatactgacatgcaagagtttgatcaagcaattcagc	2160
Dp	2101	taggaacttcaaaagcactctgagatatactgacatgcaagagtttgatcaagcaattcagc	2160
QY	2161	atctctgaagaagcctatgctgtttcatagctctgcagcacaacaatcatcaaggaggtg	2220
Dp	2161	atctctgaagaagcctatgctgtttcatagctctgcagcacaacaatcatcaaggaggtg	2220
QY	2221	aaagagatcgatcatctatgctcttcgagaagggaacctcgcttttcttattcaatttcat	2280
Dp	2221	aaagagatcgatcatctatgctcttcgagaagggaacctcgcttttcttattcaatttcat	2280
QY	2281	ggactagcagctattcggtattaccgggttgctgctttaaagccaggaagtacaagtag	2340
Dp	2281	ggactagcagctattcggtattaccgggttgctgctttaaagccaggaagtacaagtag	2340
QY	2341	tcttgagatcaagatgaccccttgcttggagagctcttgccagcgctctagatgataagac	2400
Dp	2341	tcttgagatcaagatgaccccttgcttggagagctcttgccagcgctctagatgataagac	2400
QY	2401	acttcaagctttgaaagggttgatcaagataaccggcgctcgactccctcaatggtacacaacat	2460
Dp	2401	acttcaagctttgaaagggttgatcaagataaccggcgctcgactccctcaatggtacacaacat	2460
QY	2461	gtagaacacgacgtgactcaatgctctttagcttggaagatgaaagtggagagatgaattvgaacctg	2520
Dp	2461	gtagaacacgacgtgactcaatgctctttagcttggaagatgaaagtggagagatgaattvgaacctg	2520
QY	2521	tcgcgcggttaagagatatctcttaacaacaagttcttgagaagaagatgaccttatgacct	2580
Dp	2521	tcgcgcggttaagagatatctcttaacaacaagttcttgagaagaagatgaccttatgacct	2580
QY	2581	ccatgcttcatctcgtcttgtaacgaaatataattagacctaatatttgatgctacgctcct	2640
Dp	2581	ccatgcttcatctcgtcttgtaacgaaatataattagacctaatatttgatgctacgctcct	2640
QY	2641	ggcagattcccatctcgtcttcttggtatttggtgataatataaacttaataaagaacaa	2700
Dp	2641	ggcagattcccatctcgtcttcttggtatttggtgataatataaacttaataaagaacaa	2700
QY	2701	taggaagaacgacgggttcaatgctctgacctccatcatcatagggagctcaagacctccaac	2760
Dp	2701	taggaagaacgacgggttcaatgctctgacctccatcatcatagggagctcaagacctccaac	2760
QY	2761	cataaattctcaagctcgctcggttctggtatgtaattgtaagtgttaatttggaattttaa	2820
Dp	2761	cataaattctcaagctcgctcggttctggtatgtaattgtaagtgttaatttggaattttaa	2820
QY	2821	ttatcatgatcgctgctgagatgctgaactacatgacaatttggatatactgccaacgagagatt	2880
Dp	2821	ttatcatgatcgctgctgagatgctgaactacatgacaatttggatatactgccaacgagagatt	2880
QY	2881	taagttttaaaaaaaaaaaaaaaaaaattccatg	2913
Dp	2881	taagttttaaaaaaaaaaaaaaaaaaattccatg	2913

RESULT	2
AAV38720	
ID	AAV38720 standard; DNA; 3090 BP

Query Match	Best Local Similarity	Score	DB	Length
Matches 2254; Conservative	88.3%;	2028;	19;	3090;
	0;	Mismatches	285;	Indels 15; Gaps
1 cctctcaactctcagcgaatggaacacccatcatcagaatcgtttctctgtg 60				
111 cttctcaactctcagcgaatggtatctactacactgtatcagcatcgtttctgtg 170				
61 ---ctccactctgcaaatctcaatctacgcggttcacatggtctcgtggaagactctctt 117				
171 cactctcaactctcaaatctcaatctcagcagctctcattcgtcgtggaagactctctt 230				
118 gcttctcttcaactt---caagagagcgtttctcaggaaggtctctctcgtggaatcat 174				
231 gcttctcttctcctctggaagagagctgtttctcgtggaagatcttgcgtggaagtcct 290				
175 ctatgaatctgacccctcaaatgtaatggtcactgctcttaagaagctc---ttccgtg 231				
291 ctatgactgctgctcctcaaatcttactctctcgtcatctggaaggtctctgttctctg 350				
232 atggtcgtatgtaatgctatcttcttccacagatcaaatggaagcccccgtgacagttt 291				
351 atgatacagatggtgctctcttcttccacacatcatcattagaagaccactggaacagttt 410				

DB 2571 tggatatagcaccatctagagacagcagtgctctatgcttagttagaagaatgaagaatg 2630

QY 2506 atgaattggaacctgtgcgcggttaagatatc 2539
DB 2631 aagcagagaatgaagtagaagtgaaatgaacc 2664

RESULT 3

ID AAT69587 standard; cDNA; 3074 BP.

AC AAT69587;

DT 26-AUG-1997 (first entry)

DE Potato starch branching enzyme II gene (beII).

KW Starch branching enzyme II; beII gene; potato; transgenic plant;

XX amylopectin; amylose; starch; ss.

OS Solanum tuberosum.

XX Key Location/Qualifiers

FH CDS 189..2825

FT sig_peptide 189..332

FT mat_peptide 333..2822

FT /*tag= c

PN WO9720040-A1.

XX 05-JUN-1997.

PF 28-NOV-1996; 96WO-SE01558.

PR 19-APR-1996; 96SE-0001506.

PR 29-NOV-1995; 95SE-0004272.

XX (EKBB/) EK B.

PA (KHOS/) KHOSNOODI J.

PA (LARS/) LARSSON C.

PA (LARS/) LARSSON H.

PA (RASK/) RASK L.

PA (AMTL-) AMTLOGENE HB.

XX Ek B, Khosnoodi J, Larsson C, Larsson H, Rask L;

XX MPI; 1997-310596/28.

DR P-PSDB; AAM19113.

XX Isolated potato starch branching enzyme II - useful for altering

PT degree of amylopectin branching and amylopectin/amylose ratio in

PT potato starch

XX Claim 4; Page 12-15; 24pp; English.

PS A cDNA clone (AAT69587) codes for potato starch branching enzyme II

CC (BEII) (AAM19113). It was isolated from potato tuber cDNA by PCR

CC amplification using primers (AAT69588-89) based on tryptic peptides

CC of isolated BEII; the 5' and 3' ends of the sequence were deltd. by

CC RACE. A vector comprising the whole or a functional active part of

CC the isolated sequence (sense or antisense), plus regulatory

CC sequences active in potato, can be used to produce transgenic

CC potatoes. The starch obtd. from such plants will show a changed

CC pattern of amylopectin branching and an altered amylopectin/amylose

CC ratio.

XX Sequence 3074 BP, 902 A; 560 C; 710 G; 896 T; 6 other;

Query Match

47.5%; Score 1384; DB 18; Length 3074;

Best Local Similarity 76.7%; Pred. No. 0;
Matches 1690; Conservative 0; Mismatches 514; Indels 0; Gaps 0;

QY 347 tgttgaagatgaagtaataagaatcgttccaatgcyggagacagttagatcagaaga 406
DB 617 tggtaacttgagagagctaaacatlaacttctgaagagacaattatgtatgac 676
QY 407 aattggtctaaaccaaaggtccattctccaccgagcagaagatataatgact 466
DB 677 tgaatgatacagaagaggggacatccaccactgtgacttgcagaagattatgaat 736
QY 467 agatccaaagcttgcagagcttctgcacacactagattacaggtatccaaagaa 526
DB 737 agacccttttgacaacactatcgtcaacacacttgattacaggtatccaaagaa 796
QY 527 actccagaagaagaattgacaagatagaagtgatcgtgacttctcgtgacta 586
DB 797 actgaggaagcaattgacaagatagaagtggtgttggaagcttctcgtgtatga 856
QY 587 aaagttggttctcagcaggtgaacagaataactatagaagatggcaccagagc 646
DB 857 aaaaatggttctcagcaggtgaacagaataactatagaagatggcaccagagc 916
QY 647 taagtggcctgacttgattgagatttcaataactgaaatccaaagatgactgac 706
DB 917 ccagtcagcgtccctcacttgagatttcaacattggaagcagaatgctgactatgac 976
QY 707 tcagaatgagtggtgtgtctgtgagagatcttttccgaataatgacagatgtccacc 766
DB 977 tcggaatgaaattgtgtgtcgtgagagatcttctccaaataaagtgatgtgtctcctg 1036
QY 767 aattcccatggttctcagtgagtaagaatgacatgacatccatctgcgaacaaagact 826
DB 1037 aattcccatggttctcagtgagtaagaatgacatgacatccatctgcgaacaaagact 1096
QY 827 tattcgtcttgatcaagcttccagtcagcagcaggtgaactccatataatgacat 886
DB 1097 cattccgtcttgatcaagcttccagtcagcagcaggtgaactccatataatgacat 1156
QY 887 atactatgactcccgagagagagaagatgtgttcaaaaatccctcagccaaagagcc 946
DB 1157 atactatgactcccgagagagagaagatgtgttcaaaaatccctcagccaaagagcc 1216
QY 947 aaaaactcctcggttatagatgcacggttggaatgagatgacgagccagtaataa 1006
DB 1217 aaagtcgtgagaatataatgacatctatctggaatgagatgacgagccagtaataa 1276
QY 1007 cacatagccaactttagaagatgagtggtcttccgcacataaaaagcttgatcaatgc 1066
DB 1277 ctcatagtgagatatttagaagatgagtggtcttccgcacataaaaagcttgatcaatgc 1336
QY 1067 tgttcagctatgctatttcaagaagacatcatatgactgatttggatatacgtcac 1126
DB 1337 ggttcaaatatgctatttcaagaagacatcttattatgctgatttggatatacgtcac 1396
QY 1127 aaactttatgagcgtcagcagcagcttcttgaactccgagatttaagttcctaataa 1186
DB 1397 aaactttatgagcagcagcagcagcttcttgaactccgagatttaagttcctaataa 1456
QY 1187 taaagtcagagatgagtggtcttcttccatagatataatgctatgacatgacatgac 1246
DB 1457 taaagtcagagatgagtggtcttcttccatagatataatgctatgacatgacatgac 1516
QY 1247 taataagcttgagtggtcgtatagatggttgaagtaagagatgacatgacttcaactcgtg 1306
DB 1517 taataagcttgagtggtcgtatagatggttgaagtaagagatgacatgacttcaactcgtg 1576
QY 1307 acccaggggtatcagatgagtggtgagcttgccttcaactatgagagagcgtggagagt 1366
DB 1577 agctcgtggtatcagatgagtggtgagcttgccttcaactatgagagagcgtggagagt 1636
QY 1367 tctaaggttcttcttcaactatgagtggtgagcttgccttcaactatgagagagcgtggagagt 1426

QY 1847 ggaagagatagatgacttcatgctcttgacagaccatctctcatatcg 1906
 |||||||
 DB 1843 ggaagagatagatgacttcatgctcttgacagaccatctctcatatcg 1902
 QY 1907 tggagtagcatgacaaatgacatcagcttatcatcagtggaagcggaagata 1966
 |||||||
 DB 1903 tggagtagcatgacaaatgacatcagcttatcatcagtggaagcggaagata 1962
 QY 1967 ttgaattttggaatgaaatttgacaccccgagtgatgatttcccaagata 2026
 |||||||
 DB 1963 cctaatttcatggaatgaaatttgacaccccgagtgatgatttcccaagata 2022
 QY 2027 tctgacttcccgagtgatgaaatttgcctcggaacaattacaggttatgaaatcg 2086
 |||||||
 DB 2023 rcaaacactctctgagtgctcagtaattcccggaacacacacacacacacacac 2082
 QY 2087 gctgagtgtagttagcagcatcagaacatcagatagatagatgaaatgaaatgaa 2146
 |||||||
 DB 2083 acgagagattgacactcgagatgacagatatttaagatagatgagtggaagatttga 2142
 QY 2147 tcaagcaattcagcatccttgagaagacgctatgcttcatgactctgagacacacat 2206
 |||||||
 DB 2143 ccgggcttagttagttagttagttagttagttagttagttagttagttagttagttagt 2202
 QY 2207 atcagagagatgaaagagagatgacatgcttctcgagaggggaacccgcttctgt 2266
 |||||||
 DB 2203 atcagagagatgaaagagagatgacatgcttctcgagaggggaacccgcttctgt 2262
 QY 2267 attcaatttcatgagatcagcatccttgagatcagcatcagatgctgctgtaagcag 2326
 |||||||
 DB 2263 cttaatttcatgagatcagcatccttgagatcagcatcagatgctgctgtaagcag 2322
 QY 2327 aaagcaagatgcttctgagatcagcatccttgagatcagcatcagatgctgctgta 2386
 |||||||
 DB 2323 aaagcaagatgcttctgagatcagcatccttgagatcagcatcagatgctgctgta 2382
 QY 2387 tcatgagatcagcatccttgagatcagcatccttgagatcagcatcagatgctgctgta 2446
 |||||||
 DB 2383 tcatgagatcagcatccttgagatcagcatccttgagatcagcatcagatgctgctgta 2442
 QY 2447 ggtgacacacatgtagaagacagtggtcctgagtgtagtggaagtggaagtggaag 2506
 |||||||
 DB 2443 ggtgacacacatgtagaagacagtggtcctgagtgtagtggaagtggaagtggaag 2502
 QY 2507 tgaattggaacctgctgcgcgttaa 2531
 |||||
 DB 2503 agaagaagaagaancgmgagaaga 2527

 RESULT 6
 AAT42632
 ID AAT42632 standard; DNA; 3231 BP.
 XX
 AC AAT42632;
 XX
 DT 25-FEB-1997 (first entry)
 XX
 DE Class A starch branching enzyme (psbe2con.seq).
 XX
 KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
 XX amylose; viscosity; potato; ss.
 OS Solanum tuberosum.
 XX
 FH Key Location/Qualifiers
 FT misc_RNA 45..3200
 FT /*tag= a
 FT /*note= "Claim 34"
 FT CDS 228..2855
 FT /*tag= c
 XX
 PN W09634968-A2.

PD 07-NOV-1996.
 XX
 PF 03-MAY-1996; 96WO-GB01075.
 XX
 PR 10-APR-1996; 96GB-0007409.
 PR 05-MAY-1995; 95GB-0009229.
 XX
 PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX
 PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
 PI Sidebottom CM, Westcott RJ;
 XX
 DR WPI: 1996-506170/50.
 XX
 PT New potato plant starch having high amylose content - also class A
 PT starch branching enzyme and corresp. DNA to alter the viscosity of
 PT starch; for use in food, biodegradable products, adhesives, etc.
 XX
 PS Claim 31, 34; Page 53-55; 142pp; English.
 XX
 CC Class A starch branching enzyme (SBE) has been obtained from
 CC potatoes. In class A SBE mols., a flexible N-terminal domain,
 CC is found, which is not found in class B mols.
 CC The same sequence is given in Figure 8, however, nucleotides
 CC 1-44 omitted.
 XX
 SQ Sequence 3231 BP; 960 A; 577 C; 739 G; 947 T; 8 other;

 Query Match 47.3%; Score 1377.8; DB 17; Length 3231;
 Best Local Similarity 76.1%; Pred. No. 0;
 Matches 1694; Conservative 2; Mismatches 529; Indels 0; Gaps 0;

 QY 347 ttttgaagatgaagtaataaagaatctgttccaatgcygggagacgttagatcagaa 406
 |||||
 DB 656 tggtaaatgag 715
 QY 407 aattgagatcag 466
 |||||
 DB 716 tgaatagatag 775
 QY 467 agatcag 526
 |||||
 DB 776 ag 835
 QY 527 actcag 586
 |||||
 DB 836 aatgag 895
 QY 587 aagattggttctcag 646
 |||||
 DB 896 aaaaatggttctcag 955
 QY 647 taagtggctgagatgag 706
 |||||
 DB 956 ccaagtcag 1015
 QY 707 tcaagatgagtggt 766
 |||||
 DB 1016 tcaagatgagtggt 1075
 QY 767 aattcccaagtggtctcag 826
 |||||
 DB 1076 aattcccaagtggtctcag 1135
 QY 827 tattcctgtgtagtaag 886
 |||||
 DB 1136 cattcctgtgtagtaag 1195
 QY 887 atactatgagatcctcag 946
 |||||
 DB 1196 atactatgagatcctcag 1255

PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147312.
 PR 05-AUG-1999; 99US-0147320.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149375.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.

PR 29-OCT-1999; 99US-0162142.
 Query Match 47.1%; Score 1371.4; DB 21; Length 2715;
 Best Local Similarity 72.4%; Pred. No. 0;
 Matches 1837; Conservative 0; Mismatches 666; Indels 36; Gaps 3;
 QY 144 ttctctagaggggtctctctctgtgaagctcatcgaatctgaactcccaatgaatg 203
 Db 136 tctcttggaaggttttctgtcgaagccatcgtatgatcttgatctgccttcctagct 195
 QY 204 gtcaactgtctctaaagagctcctcctgtatgctggaattgaatgctatcttcctcaaca 263
 Db 196 accactgcatctgagaagctccgttgccca---tcagatgatagtccttcctcatgctct 252
 QY 264 gatcaattggaagccctctgcaagatttgaagaatcccaagttgcttactatggttgag 323
 Db 253 gatcaagtaacaatcccggaatcgtctcgaacatactcaagttgctggaactgtagac 312
 QY 324 agtctcatltagatgaataagattgttgaagatcgaatgaataaagaatctg---ttcc 379
 Db 313 gtccagaanaactgaagaagccaggaacagacactgatcaactctgcactctca 372
 QY 380 aatgcyggaagacgttagacatcagaanaaatt----- 410
 Db 373 acatctggaagcataagttataagaagatttgcagaagatgcacactctgacacca 432
 QY 411 gstatcaaccaaggtccatctcctccacccgagagggcaagaatataatagat 470
 Db 433 gaagttggaaggaagatccacccctcctggaatggaagaaatataatgacattgat 492
 QY 471 ccaagctgacagcttctcgtcaacacactagattacccgtatccaagtaacagaacaccc 530
 Db 493 cctatgttgaacagctcatcgtatcatctctgattacccgatatggaagtaacagaacacg 552
 QY 531 cgagaagaanaattgacaagttgaagtagtctggaatcttctcgtggtctatgaaag 590
 Db 553 cgttaagaanaattgacaagaatggaagtgtgttggaagcatttctcgttgattgaata 612
 QY 591 ttggtttccacgcagttgaacagaataacttatagagatgggcaccagagtagag 650
 Db 613 ttggtctcaactcgaagcgcactggtatcatcactccggaatgggcaccggaagtagag 672
 QY 651 tgggtcgtatgtattggaatttcaataactggaatccatcaatgcaatgcaatgacatcg 710
 Db 673 gcagcatcactgctcggagatttataaactggaatgccaactctgattttagtgcgtg 732
 QY 711 aatgagtgtgtgtctgtggaagatcttctgcgaataatgacagatggttcacccaaatt 770
 Db 733 aacgacttgtgtgtggaataatattctgcgaataatgctgatatggttcacccaaatt 792
 QY 771 ccccatggtctcgcagtaagaatgacgcatgatactccatctgccaacaaagattctatt 830
 Db 793 ccccatggtctcgcgtgtggaagatcgcgcatgatacccatctggtatttaagaactcatt 852
 QY 831 cctgcttgaataagttcagttccaagcacagcagtggaactcccatcatalaattgcatatcc 890
 Db 853 ccagcttgatcaagttatctgtccagccacctcggcgagatcccatatataatgagatatt 912
 QY 891 tatgatactcccgaggaaggaatgtagtgttcaaaaatccctcagccaagaagaccaaa 950
 Db 913 tatgacctccttgagggaggaataatgtagtgcataacatccctgcgtccaagaagaaccaca 972
 QY 951 tcaactcggattatagatgtgcacggttgggaatgagtagtgcaggaacagtaataaacaca 1010
 Db 973 tgcgtgcgtatataatgatacatcattgtggaatgagtagtgcaggaacagtaataataaca 1032
 QY 1011 tatgccaactttagagatgtagtctcctccgcatccaanaagcttgccaactggtgt 1070
 Db 1033 tatgccaactttagagatgtagtctcctccgcatccaanaagcttagctataatggtgtg 1092
 QY 1071 cagctcatggtatccaagacatcataatgctagtttggatatacgtcacaaac 1130
 Db 1093 cagtaatggcatccaagacatgctactatgccaagcttggatcatgataatgacaaat 1152

QY 1131 tttaacagctagcagccgatttggaactcctgattttaaagctctaagataa 1190
 Db 1153 ttlttcgacactagcagccgcttllggaacacccgatggaacttaactttagagacaaa 1212
 QY 1191 gccacagatgactgtctctgttctcaatgatatgttcacatgcatcaactaat 1250
 Db 1213 gccatagagctagctcgtgtgtctcgatgatatgtgacacgcatgatacaaaaac 1272
 QY 1251 acgtttagatgagctgataatgatttgatgacgagtgatcacttcaactctgacaa 1310
 Db 1273 acactggaatgcccgcgacagatctgagacgagtgatcaacttcaactctgagatcg 1332
 QY 1311 cggaggtacatcagatgagtggaactcgccttcaactaagagcgctggagagttcta 1370
 Db 1333 cgtgtatcatcagatgagtgagatctcgtcttcaactaagagcgctggagagttcgt 1392
 QY 1371 aggttctcttcaaatgacagagtggtgttgatgagatgacagttgagtgatcaga 1430
 Db 1393 aggtatctcttcccaacgagagatggtgttgagaaatgacagttgagtgatcaga 1452
 QY 1431 ttgtagatgagtgacatcagatgacagcagatgagatgagtgagtgatcaga 1490
 Db 1453 ttgtagatgagtgacatcagatgacagcagatgagatgagtgagtgatcaga 1512
 QY 1491 aacacacataactctgatatgacatgacatgacatgacatgacatgacatgacatgac 1550
 Db 1513 aattacacataactctgatatgacatgacatgacatgacatgacatgacatgacatgac 1572
 QY 1551 ttgtagatgagtgacatcagatgacagcagatgagatgagtgagtgatcaga 1610
 Db 1573 gtagagatgagtgacatcagatgacagcagatgagatgagtgagtgatcaga 1632
 QY 1611 ggaatgcacacagcttgacatcagatgacagcagatgagatgagtgagtgatcaga 1670
 Db 1633 ggaatgcacacagcttgacatcagatgacagcagatgagatgagtgagtgatcaga 1692
 QY 1671 cacaatgagctgtctgataaaatgagtgagtgatgagtgagtgagtgagtgagtgag 1730
 Db 1693 cacaatgagctgtctgataaaatgagtgagtgatgagtgagtgagtgagtgagtgag 1752
 QY 1731 atgagtgacatctgataaaatgagtgagtgatgagtgagtgagtgagtgagtgag 1790
 Db 1753 atgagtgacatctgataaaatgagtgagtgatgagtgagtgagtgagtgagtgag 1812
 QY 1791 gctgaaagctgacacagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1850
 Db 1813 gctgaaagctgacacagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1872
 QY 1851 aaggaatgagtgacatcagatgacagcagctgtgtgtgtgtgtgtgtgtgtgtgt 1910
 Db 1873 aaggaatgagtgacatcagatgacagcagctgtgtgtgtgtgtgtgtgtgtgtgt 1932
 QY 1911 gtagcattgacacacagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1970
 Db 1933 atgcttcaacacacagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1992
 QY 1971 aattttaggaaatgaaatgagtgacaccccgagtgagtgagtgagtgagtgagtgag 2030
 Db 1993 aattttaggaaatgaaatgagtgacaccccgagtgagtgagtgagtgagtgagtgag 2052
 QY 2031 catctcccgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2090
 Db 2053 catctcccgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2112
 QY 2091 aggtttagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2150
 Db 2113 aggtttagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2172
 QY 2151 gcaatcagatctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2210
 Db 2173 gcaatcagatctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2232

QY 2211 cggagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2270
 Db 2233 cggagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2292
 QY 2271 aattttagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2330
 Db 2293 aattttagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2352
 QY 2331 tacaagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2390
 Db 2353 tacaagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2412
 QY 2391 gatcagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2450
 Db 2413 gatcagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2472
 QY 2451 tacaacacatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2510
 Db 2473 tacaacacatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2532
 QY 2511 ttggaacgtgtgcggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2570
 Db 2533 ttggaacgtgtgcggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2592
 QY 2571 tatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2630
 Db 2593 tatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2652
 QY 2631 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2690
 Db 2653 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2712
 QY 2691 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2750
 Db 2713 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2772
 QY 2751 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2810
 Db 2773 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2832
 QY 2811 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2870
 Db 2833 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2892
 QY 2871 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2930
 Db 2893 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2952
 QY 2931 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2990
 Db 2953 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3012
 QY 2991 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3050
 Db 3013 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3072
 QY 3051 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3090
 Db 3073 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3112
 QY 3091 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3150
 Db 3113 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3172
 QY 3151 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3210
 Db 3173 cagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 3232

RESULT 9

AA142636

ID AA142636 standard; DNA: 2576 BP.

AA142636;

03-MAR-1997 (first entry)

Class A starch branching enzyme (86con.seq) cloned in Q632.

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;

amylose; viscosity; potato; ss.

Solanum tuberosum.

WO9634968-A2.

03-MAY-1996; 96WO-GB01075.

10-APR-1996; 96GB-0007409.

05-MAY-1995; 95GB-0009229.

(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;

Slidebottom CM, Westcott RJ;

WPI: 1996-506170/50.

New potato plant starch having high amylose content - also class A

starch branching enzyme and corresp. DNA to alter the viscosity of

starch; for use in food, biodegradable products, adhesives, etc.

Example 1; Page 49-51; 142pp; English.

Class A starch branching enzyme (SBE) has been obtained from

potatoes. In class A SBE mols., a flexible N-terminal domain,

is found, which is not found in class B mols.

Db 2388 tcataatgcgaatattccacttgaagatgtagatgatcgtccgttcaattat 2447
 QY 2447 ggtgtacaacacatgtagaagaagatgtagatgtagatgtagatgtaga 2506
 Db 2448 ggtgtacaacacatgtagaagaagatgtagatgtagatgtagatgtaga 2507
 QY 2507 tgaattgaa 2516
 Db 2508 agaagaagaa 2517

RESULT 10
 ID AAT42630 standard; DNM: 3033 BP.
 AC AAT42630;
 XX 25-FEB-1997 (first entry)
 DE Class A starch branching enzyme (19con.seq).
 KM Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
 KW amylose; viscosity; potato; ss.
 XX Solanum tuberosum.
 OS
 XX Key Location/Qualifiers
 FH CDS 145..2793
 FT sig.peptide /*tag- a
 FT 145..288
 FT mat.peptide /*tag- b
 FT 289..2790
 FT /*tag- c
 XX W09634968-A2.
 XX 07-NOV-1996.
 XX 03-MAY-1996; 96MO-GB01075.
 XX 10-APR-1996; 96GB-0007409.
 XX 05-MAY-1995; 95GB-0009229.
 XX (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
 PI Sidebottom CM, Westcott RJ;
 XX WPI: 1996-506170/50.
 XX P-PSDB: AAM06399.
 XX New potato plant starch having high amylose content - also class A
 PT starch branching enzyme and corresp. DNA to alter the viscosity of
 PT starch; for use in food, biodegradable products, adhesives, etc.
 XX
 PS Claim 28-30; Page 42-46; 142pp; English.
 CC Class A starch branching enzyme (SBE) has been obtained from
 CC potatoes. In class A SBE mols., a flexible N-terminal domain,
 CC is found, which is not found in class B mols.
 CC
 SQ Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;

Query Match 46.8%; Score 1364; DB 17; Length 3033;
 Best Local Similarity 75.9%; Pred. No. 0;
 Matches 1685; Conservative 0; Mismatches 535; Indels 0; Gaps 0;

QY 347 tgttgaagatgaagtaataaagaatcgttccaatgcgggaagacagttagatcaga 406
 Db 573 tgttaacatgagagagatgaataaacttaataacttctgaagagacattatgatgaac 632
 QY 407 aattgatactaaacacagatccattccctccacccggcagagaggaatataatgacat 466

Db 633 tgaatgacagagagagagagatccctccacactgacttgctgaagaattatgaat 692
 QY 467 agatcaagactgacagagcttcttcgaacacactgaattacacgtatcaagtcacaag 526
 Db 693 agaccoccttgcacaactatcgcacacacttgattacaggtatcaacagtcacaagaa 752
 QY 527 actccagaagaagaattgcaagatgaagatgtagatgtagatgtagatgtagatgtaga 586
 Db 753 actgaagagagagacattgcaagatgaagatgtagatgtagatgtagatgtagatgtaga 812
 QY 587 aagattggttcttcacgcagatggaacagaataactatagaagatgtagatgtagatgtaga 646
 Db 813 aaaaatggttcttcacgcagatggaacagaataactatagaagatgtagatgtagatgtaga 872
 QY 647 taagtggatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 706
 Db 873 ccagtcagctgcctccatctgtagatgtagatgtagatgtagatgtagatgtagatgtaga 932
 QY 707 tgaagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 766
 Db 933 tggatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 992
 QY 767 aattcccatggttcttcacgcagatggaacagaataactatagaagatgtagatgtagatgtaga 826
 Db 993 aattcccatggttcttcacgcagatggaacagaataactatagaagatgtagatgtagatgtaga 1052
 QY 827 tattcctgctgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 886
 Db 1053 caticctgctgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1112
 QY 887 atactatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 946
 Db 1113 acatcatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1172
 QY 947 aaatcacttgcagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1006
 Db 1173 aaagtgcgtggaatataatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1232
 QY 1007 caacatgccaacttgaagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1066
 Db 1233 ctcatagtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1292
 QY 1067 tcttgcctgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1126
 Db 1293 gctgcaaatatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1352
 QY 1127 aaacttgcagtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1186
 Db 1353 aaatttttgcacacagcagcgttcttggaagccgcagacacttaagctttagatgtaga 1412
 QY 1187 taaagctgaagtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1246
 Db 1413 taaagctgaagtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1472
 QY 1247 taaagctgaagtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1306
 Db 1473 taaagctgaagtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1532
 QY 1307 accacgggtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1366
 Db 1533 agctcgtgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1592
 QY 1367 tcaaggttcttcttcacacagtagatgtagatgtagatgtagatgtagatgtagatgtaga 1426
 Db 1593 acttagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1652
 QY 1427 cagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1486
 Db 1653 tagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1712
 QY 1487 cgcacacacagtagatgtagatgtagatgtagatgtagatgtagatgtagatgtagatgtaga 1546

Dd	1713	tgaggaaactagaggaaactatttggaactgcgaactgaatgtgatactgtctgttgcattccgat	1772
Qy	1547	gctgttgatgatgatgtatcattgatgtctctctccagaaggtgtgcacacattgtgtgaagatgt	1606
Dd	1773	gctgttcaacagatcattattcattggtcttctccagaatgcgaattacacattgtgtgaagatgt	1832
Qy	1607	taagtgtgaatgccaaacgatttgcttcccggttgaagaatgtgtgtgttgcatttgataatcg	1666
Dd	1833	taagcgaatgtccgaacatttgttatctccgcgccaaaggggggtgtgttgcatttgataatcg	1892
Qy	1667	tctccacatgctgtctgtcgtataaaggggtttagatattatctccagaagagaatgtgaagattg	1726
Dd	1893	gctgtcatatggtcaattgtcgtataaagcgatgtgaatgtgtctccaaagaacgggtatggatgtg	1952
Qy	1727	gaaaaatgtgtacatgtgtatatacatgtctgtgaacccaagcggtgtgtgtgaagaagtgtttcc	1786
Dd	1953	gagagtggtgtatattgtttcatacactgtgacaaatagaagatgtgtcgaagaagtgtgtttcc	2012
Qy	1787	ttatgtcgtgaagatgcataccagagccctttgttgtaacaaacatattgcatatttgctgcgat	1846
Dd	2013	atacgcgtgaagatgcatacgaacgtccctagtcggtgtgaataacatacagatcttcgtcgat	2072
Qy	1847	ggacaagagatatgtatgacttcaatgtgctctgtgaacagacatctacatccctccatagatcg	1906
Dd	2073	ggacaagagatatgtatgattttatgtgctctgtgatagaccgtcaacatcattatgatatgcg	2132
Qy	1907	tgtgagtatgcattgcacaaaatgtacaggtcttataccatgggatttaaggcggagaagata	1966
Dd	2133	tgtgagtatgcattgtgacaaagatgtattgagctgtgtaaatacgtgatttagagagagaaggtta	2192
Qy	1967	tttgatatttatgtgaaatgaataatttggaaccccggtgtgattgtttccaaagagtga	2026
Dd	2193	ctctaatttcatgttggaatgtgaatttgcgcacccgtgagtgatgtgtttcccttaggtctga	2252
Qy	2027	tctacatcttcccaagtgtgtaaattgtctccctgttggaacaaattacagttatgtataatgcg	2086
Dd	2253	acaacacactctctgtatgtgtccagtaatcccggaacccaattcagttatgtataaatgcag	2312
Qy	2087	ggcgtaggtttgatcttaagtcgaatccaagatcctcgaaatctcgaatctcgtgaatgcgaagtttga	2146
Dd	2313	acggagatatttgaccctgtgagatgcgaataataatgaatacgcgtgtgtgtgcgaagaatttga	2372
Qy	2147	tcaagcaatttgaagatctgtgaagaagccctatggtttcattgatcattctgtgcacacatacat	2206
Dd	2373	ccggcctatgcagatcttgaagaataatagataggtttatgacttcagaacacgattcat	2432
Qy	2207	atcacggaaagatgaagaaggtatcgatcatatgtctctcgagaaggggaaacctcgttttgt	2266
Dd	2433	atccgaaagagatgaagaagatagatgattgtatttgaataaaggaacccatgattttgt	2492
Qy	2267	atlaaatttcaattgtgagctgcagcattcccgattccggaatccgaagtgtgccttgaagccgg	2326
Dd	2493	cttaatttcttcaactgtgcgaanaaagcatttccagagactatgcataagcgtgcctgtgaacctgg	2552
Qy	2327	aaagtacaaagatgacttctgtgatttcagaatgatacccttgttttggaagccttvtgcagcgctag	2386
Dd	2553	aaaatacaaggttctgttgatccagatgatacccaactttgtgtgcctcgggagaaattga	2612
Qy	2387	tcatatgtgcagagacttcaagctttgaaggtgtgtacgtataccggctcgatccctcat	2446
Dd	2613	tcatatgtgcgaataatttccacttgaagagatgtatgtatgtatgcctccgtcttcaatat	2672
Qy	2447	ggctgtacaacacatgtatgaacacagatgtgtcctatgcttgaatgtgagagatgaatgtgaaga	2506
Dd	2673	ggctgtatgcacctgttgaanaacagcaggtgtctatgtacactatgtagaacaaagaagaaga	2732
Qy	2507	tgaatttgaacctgtgcgcggttgaagatatatcttaacaacaggttctgtgaacgagatgt	2566
Dd	2733	agaagaagaagaagaagaagaatgaacgaacgaatgaagaagaatgaatgaatgaagaagaatgt	2792

RESULT 11
AAT42634

ID	AAAT42634 standard; DNA; 3003 BP.
XX	
AC	AAT42634;
XX	
DT	03-MAR-1997 (first entry)
XX	
DE	Class A starch branching enzyme (10con.seq).
XX	
KW	Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KM	amylose; viscosity; potato; ss.
XX	
OS	Solanum tuberosum.
XX	
PN	MO9634968-AZ.
XX	
PD	07-NOV-1996.
XX	
PF	03-MAY-1996; 96MO-GB01075.
XX	
PR	10-APR-1996; 96GB-0007409.
XX	
PR	05-MAY-1995; 95GB-0009229.
XX	
PA	(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX	
PI	Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI	Siebottom CM, Westcott RJ;
XX	
DR	WPT; 1996-506170/50.
XX	
PT	New potato plant starch having high amylose content - also class A
PT	starch branching enzyme and corresp. DNA to alter the viscosity of
PT	starch; for use in food, biodegradable products, adhesives, etc.
XX	
PS	Example 1; Page 38-39; 142pp; English.
XX	
CC	Class A starch branching enzyme (SBE) has been obtained from
CC	potatoes. In class A SBE mols., a flexible N-terminal domain,
CC	is found, which is not found in class B mols.
XX	
SQ	Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;

1.

QY 767 aatccccatggtctcagataaagatagacatgagatccatctgagcaacaagattc 826
 Db 991 aatccccatggtccagatagatagatacctgagacacccatcaagttcttaagattc 1050
 QY 827 tattccgtcttgatcaagtctcagttcaagcaacagatggaactcccatataatgcat 886
 Db 1051 catcccgctctgagatcaacaccccttcaacagctcccgatggaatcttcaataatggaat 1110
 QY 887 atactatgacctccgagagaggaagtatggttcaaaaactcccaagcaagagacc 946
 Db 1111 atataatgataccaccgaagagagagatatacttcccaacaccgagcaagaagacc 1170
 QY 947 aaaaatcctcogataattatagtcagtcagcttggaatgagtagtaagagccagtaataa 1006
 Db 1171 aaagtcggtagaaatataatataatctcatatggaatgagtagtcggagcctaataa 1230
 QY 1007 cacatacgcaactttagagatgagatggtcttcctcgcat-caaaaagcttgatcaatg 1065
 Db 1231 ctctacagtggaatttagagatgagatggtcttcctcgcatataaaaagcttgatcaatg 1290
 QY 1066 ctgtcagcaactgagctattccaagaagatccatataatgtagttttggatcacagctca 1125
 Db 1291 cgtgcaaatatagctattccaagaagatccatataatgtagttttggatcacagctca 1350
 QY 1126 caaaacttttag 1185
 Db 1351 caaaacttttttgcacacag 1410
 QY 1186 ataaagctcagagatgagatggtcttccttcctcatgataatggttcatagcaatgataa 1245
 Db 1411 ataaagctcagagatgagatggtcttccttcctcatgataatggttcatagcaatgataa 1470
 QY 1246 ctatagctgagatgag 1305
 Db 1471 atataatcttag 1530
 QY 1306 gacacagagagatcagatgagatgagagagagagagagagagagagagagagagagagag 1365
 Db 1531 gagctcgtctctcatcagatgagatgagagagagagagagagagagagagagagagagagag 1590
 QY 1366 ttctaaagttctctctctcaaatgagagagagagagagagagagagagagagagagagag 1425
 Db 1591 tacttagtatactctctcaaatgagagagagagagagagagagagagagagagagagagag 1650
 QY 1426 tccagatttgatgag 1485
 Db 1651 ttgatttgatgag 1710
 QY 1486 ccgagcaactcaaatgagatcttgcagataatgagagagagagagagagagagagagagag 1545
 Db 1711 ctggagacactcag 1770
 QY 1546 tgcgttgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1605
 Db 1771 tgcgttgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1830
 QY 1606 ttgattgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1665
 Db 1831 ttgattgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1890
 QY 1666 gtctcagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1725
 Db 1891 gtctcagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1950
 QY 1726 ggaataatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1785
 Db 1951 ggaataatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2010
 QY 1786 cttaatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1845
 Db 2011 catacgtgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2070

QY 1846 tagaagaagatataatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1905
 Db 2071 tagaagaagatataatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2130
 QY 1906 gtagagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1965
 Db 2131 gtagagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2190
 QY 1966 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2025
 Db 2191 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2250
 QY 2026 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2085
 Db 2251 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2310
 QY 2086 gtagagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2145
 Db 2311 gtagagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2370
 QY 2146 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2205
 Db 2371 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2430
 QY 2206 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2265
 Db 2431 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2490
 QY 2266 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2325
 Db 2491 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2550
 QY 2326 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2385
 Db 2551 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2610
 QY 2386 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2445
 Db 2611 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2670
 QY 2446 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2505
 Db 2671 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2730
 QY 2506 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2550
 Db 2731 attgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 2775

RESULT 12
 AAT42635 standard; DNA; 2975 BP.
 AC AAT42635:
 DN 03-MAR-1997 (first entry)
 XX
 XX Class A starch branching enzyme (11com.seq).
 DE Starch branching enzyme; SBE; class A; Solanum tuberosum.
 XX amylose; viscosity; potato; ss.
 KW Solanum tuberosum.
 OS
 PN WO9634968-A2.
 PD 07-NOV-1996.
 XX
 XX 03-MAY-1996; 96WO-GB01075.
 PF 10-APR-1996; 96GB-0007409.
 PR 05-MAY-1995; 95GB-0009229.
 XX

Db 2371 ctggcgatcgatgattcttgaaataatgtatgtatgacttcgaacacagcttcac 2430
 QY 2207 atccggaagagatgaagagatcgatcattgcttcgaaagggaacactgtttt 2266
 Db 2431 atccggaagagatgaagagatcgatcattgcttcgaaagggaacactgtttt 2490
 QY 2267 atcaatttcattgactgacgacttcttcgattaccgaagtgtgctttaaagcag 2326
 Db 2491 cttaatttcactgacgaataatgacttcaagactacgataagctgcttgaagctcg 2550
 QY 2327 aaagtacaagaatgacttcttgattcaagatgacttcttgaggagacttggcagagcttag 2386
 Db 2551 aaataacaaggttcttcgactgaacatgacttcttcgagacttcttgagctcgagagacttag 2610
 QY 2387 tcatgacgacgagacttcttcgacttgaagggtgtgacgaacacgagcttcgacttcac 2446
 Db 2611 tcaataagccgaatattccacttcgactgaagactgactgactgactgacttcaattat 2670
 QY 2447 ggtgtacacacgactgacgaacagatgctgacttcttcgagtgagatgagatgagag 2506
 Db 2671 ggtgtacacacgactgacgaacagatgctgacttcttcgagtgagatgagatgagag 2730
 QY 2507 tgaattgaa 2516
 Db 2731 agtagtagaa 2740

RESULT 13

AA073750
 ID AA073750 standard, cDNA to mRNA, 2919 BP.

AA073750:

05-JUL-1995 (first entry)

Rice starch branching enzyme.

Starch branching enzyme; rice; starch content; ds.

Oryza sativa.

Location/Qualifiers

Key 1..127

5'UTR /*tag- a

transit_peptide 128..322

mat_peptide 323..2606

/*tag- c

/product- branching_enzyme

2603..2919

/*tag- d

3'UTR

JP06261767-A.

20-SEP-1994.

22-OCT-1993: 93JP-0265171.

29-OCT-1992: 92JP-0291719.

(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

WPI: 1994-337418/42.

P-PSDB: AAR60811.

PS Claim 1: Page 9-12: 13pp: Japanese.

XX The rice starch branching enzyme is encoded by the cDNA sequence

CC AA073750. The starch content of rice grains can be increased by

increasing the expression of branching enzyme in rice plants.

XX
 SO Sequence 2919 BP: 755 A; 590 C; 800 G; 774 T; 0 other;

Query Match 44.6%, Score 1298, DB 15; Length 2919;
 Best Local Similarity 76.5%, Pred. No. 0;
 Matches 1592: Conservative 0; Mismatches 490; Indels 0; Gaps 0;

QY 417 aaacaaaggtcattccctccaccgagagagcagaagaatataatgacataga:ccaagc 476
 Db 527 aaacaaaggttctccaccaccagaagagatgagcaaaaaatattccagatgactatg 586
 QY 477 tgaacagcttcgcgaacacactagatcaggttccacagacaaagaagctccgagaa 536
 Db 587 cttaatggtataagttacacatcttgataatcagataagcctataagagactcgttca 646
 QY 537 gaattgacaaatgaagaatgactgactgacttcttcgctgctgctgctgctgctgct 596
 Db 647 gacattgacagatgaagaagagactggaacaattcttcgctgctgctgctgctgctg 706
 QY 597 tctcaacgagcgaagaacaggaataactatagaagaatgagcagaagaagagcttggc 656
 Db 707 ttaatacaagtgctgaagagtgctacattatcgagaatgagtgctcccgagacac:tcgca 766
 QY 657 gcatgagtggagatcttaactaactggaatcttaagatgacatgacacaaatagag 716
 Db 767 gcatlagtaggtgacttcaacaaatggaatcccaatgcaagcagcagatgaagaatagag 826
 QY 717 tctgtctcgtgagagatcttctgcgaataatgacagatgcttcaacacaaat:cccacat 776
 Db 827 ttgtgttcttgagagatcttctgcgaataatgacagatgcttcaacacaaat:cccacat 886
 QY 777 ggttctcgaatgaatacgaatgatactcattctcgaacaaagaattctactcgtc 836
 Db 887 ggtcagctgttaaaagtgctgaatggaatccattctgtgataaagagattctactcgtc 946
 QY 837 tgaatcaagcttcagcttcaacgaacagctgaactcccatataatgacatata:atgat 896
 Db 947 tgaatcaagcttcagcttcaacgaacagctgaactcccatataatgacatata:atgat 1006
 QY 897 cctcccgagaggaagaatgactgttcaaaaatccctccgaagaagaagcacaatccctc 956
 Db 1007 cctcccgagaggaagaatgactgttcaaaaatccctccgaagaagaagcacaatccctc 1066
 QY 957 cggattttagatcgacagcttggaaatgagtagtgcgagccgaagcaatgaacatgagc 1016
 Db 1067 cggattttagatcgacagcttggaaatgagtagtgcgagccgaagcaatgaacatgagc 1126
 QY 1017 aactttagagatgacttccctccgaacaaagaagctgactgactgactgactgactg 1076
 Db 1127 aactttagagatgacttccctccgaacaaagaagctgactgactgactgactgactg 1186
 QY 1077 atgctattcaagaagactcattatattatgctagcttgggatacagcttcaacaa:ttttat 1136
 Db 1187 atgctattcaagaagactcattatattatgctagcttgggatacagcttcaacaa:ttttat 1246
 QY 1137 gcaagctagcagcgaattctgactcctgataatgaatcttaataagataaagctaac 1196
 Db 1247 gcaacaaagtagcttcttcgagcccaagaagatttaagtaagtaagtaagtaagctaac 1306
 QY 1197 gacttagctctctgcttccatgataatgcttcaatacagcttcaacaaatgaagctaac 1256
 Db 1307 gacttagctctctgcttccatgataatgcttcaatacagcttcaacaaatgaagctaac 1366
 QY 1257 gatgctgctgaatgacttgaatgagtagcagcttgaacttcaactcctgagcagcggggt 1316
 Db 1367 gatgctgctgaatgacttgaatgagtagcagcttgaacttcaactcctgagcagcggggt 1426
 QY 1317 catcattgagtgagactcctccttcaacatgagagctgagagcttcaagcttcat 1376
 Db 1427 catcattgagtgagactcctccttcaacatgagagctgagagcttcaagcttcat 1486
 QY 1377 ctcttcaaatgcaagtgagtggttgaatgagatacaagtttgaatgaggttcaagttgat 1436

Fri Aug 10 16:32:39 2001

us-09-297-703a-28.Aug9.rng

Page 24

Db	1960	ttatctcagaaggaatacaacacagttatgacaactgtcgtcgaagatttgactgtgtgatg	2019
Qy	2110	caaaagcctcgatatacatatggaatgcaagatgttgatcaagcaattgaactgttgaag	2169
Db	2020	cagactctctaaaglaccaacagtaacagagattgtgatacaggaatgcaactcttgagc	2079
Qy	2170	aagcctatggtttcatgactctctgagccacaaatacatatccaggaagatgaaaggtatc	2229
Db	2080	aaaatatgataatcatatbaactctgacatccacgaatataattcccgagaaacatgaaagata	2139
Qy	2230	ggaatcatgtctcttcgagaagaggaacctcgattttgtatcatcaatttcattggaactga	2289
Db	2140	aggtgattgttggttcgaaagaagagattgtgattgtgtcaactcttcacgtgcaacaa	2199
Qy	2280	gacttcgtgcttccttcgagaagaggaacctcgattttgtatcatcaatttcattggaactga	2289
Db	2200	gctattcttgacacagctatgctgtgttcgaaagcctcgaggtgtatagaatgtgtctgact	2259
Qy	2350	cagatgacacctgtgttggaagcctcttgagcgtctgactgataatgacagacatttcagct	2409
Db	2260	ccgagcgcgtgacatactgtgtgtgattttagccgaggtccatccacgcagcgcgtctcacg	2319
Qy	2410	ttgaagaggtctgatacgaacccgctcogatcaactcttgatgtaacacacattgtgaacag	2469
Db	2320	ccgactgtctcgacatgaataatagcccatatcatcttcgcgtttatacaccaagcagaacat	2379
Qy	2470	cagtgctctatgctttagtgag	2492
Db	2380	gtgtcgtctatgctccagtgag	2402

```
Search completed: August 10, 2001, 12:53:48
Job time: 6670 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2001, 11:01:18 ; Search time 86.98 Seconds
(without alignments)
6340.116 Million cell updates/sec

Title: US-09-297-703a-28

Perfect score: 2913
Sequence: 1 cctctaactctcagcgaa.....aaaacacacacacacatcatg 2913

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1382.4	47.5	3074	US-09-087-277-1	Sequence 1, Appl
2	1251.8	43.0	2725	US-08-941-445A-14	Sequence 14, Appl
3	947.4	32.5	1393	US-09-087-277-3	Sequence 3, Appl
4	633.4	21.7	2763	US-08-941-445A-16	Sequence 16, Appl
5	605.2	20.8	3128	US-08-716-449-1	Sequence 1, Appl
6	587.8	20.2	2909	US-08-104-158-1	Sequence 1, Appl
7	369	12.7	11478	US-08-981-803-29	Sequence 29, Appl
8	369	12.7	11478	US-08-983-440-29	Sequence 29, Appl
9	68.4	2.3	2426	US-08-528-026C-3	Sequence 3, Appl
10	43.2	1.5	7218	US-08-232-463-14	Sequence 14, Appl
11	41.4	1.4	1404	US-08-204-656B-1	Sequence 1, Appl
12	41.4	1.4	1404	US-08-204-656B-3	Sequence 3, Appl
13	41.4	1.4	1404	US-08-204-656B-7	Sequence 7, Appl
14	41.4	1.4	1404	US-08-470-702-1	Sequence 1, Appl
15	41.4	1.4	1404	US-08-470-702-2	Sequence 2, Appl
16	41.4	1.4	1404	US-08-470-702-4	Sequence 4, Appl
17	41.4	1.4	1404	US-08-467-831-1	Sequence 1, Appl
18	41.4	1.4	1404	US-08-467-831-2	Sequence 2, Appl
19	41.4	1.4	1404	US-08-467-831-4	Sequence 4, Appl
20	40.2	1.4	661	US-08-961-083-77	Sequence 77, Appl
21	39.8	1.4	1404	US-08-204-656B-5	Sequence 5, Appl
22	39.8	1.4	1404	US-08-470-702-3	Sequence 3, Appl
23	39.8	1.4	1404	US-08-467-831-3	Sequence 3, Appl
24	37.8	1.3	1430	US-08-276-452A-25	Sequence 25, Appl
25	37.8	1.3	1430	US-08-798-744-25	Sequence 25, Appl
26	37	1.3	1690	US-08-276-452A-24	Sequence 24, Appl
27	37	1.3	1690	US-08-798-744-24	Sequence 24, Appl

28	37	1.3	2100	US-07-927-316A-1	Sequence 1, Appl
29	35	1.2	198	PCT-US95-10668-1	Sequence 1, Appl
30	35	1.2	198	PCT-US95-10668-2	Sequence 2, Appl
31	35	1.2	7101	US-08-480-604A-9	Sequence 9, Appl
32	35	1.2	7101	US-08-405-496A-9	Sequence 9, Appl
33	34.6	1.2	1243	US-08-687-080-53	Sequence 53, Appl
34	34.6	1.2	1376	US-08-722-184-3	Sequence 3, Appl
35	34.6	1.2	1376	US-09-043-937A-7	Sequence 7, Appl
36	34.6	1.2	5893	US-08-592-126-54	Sequence 54, Appl
37	34.6	1.2	5893	US-08-687-080-44	Sequence 44, Appl
38	34	1.2	4060	US-08-164-292B-1	Sequence 1, Appl
39	34	1.2	4060	US-08-164-292B-3	Sequence 3, Appl
40	34	1.2	4060	US-08-164-292B-5	Sequence 5, Appl
41	34	1.2	4060	US-08-164-292B-7	Sequence 7, Appl
42	34	1.2	4060	US-08-845-623-1	Sequence 1, Appl
43	34	1.2	4060	US-08-845-623-3	Sequence 3, Appl
44	34	1.2	4060	US-08-845-623-5	Sequence 5, Appl
45	34	1.2	4060	US-08-845-623-7	Sequence 7, Appl

ALIGNMENTS

```

RESULT 1
US-09-087-277-1
; Sequence 1, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087, 277B
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (92)..(2156)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; FEATURE:

```

NAME/KEY: misc.feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1428)..(1430)
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
FEATURE:
NAME/KEY: misc.feature
LOCATION: (2154)..(2156)
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

Query Match 47.5%; Score 1382.4; DB 4; Length 3074;
Best Local Similarity 76.6%; Pred. No. 0;
Matches 1689; Conservative 0; Mismatches 515; Indels 0; Gaps 0;

QY 347 ttttgaagatgaagtaataagaatctgttccatgctggagagacagttagatcagaaga 406
DB 617 ttttgaagatgaagtaataagaatctgttccatgctggagagacagttatgtatgaac 676
QY 407 aattgagctaaacaaaggtcattctccacccgacagagagagagatataatgaat 466
DB 677 ttttgaagatgaagtaataagaatctgttccatgctggagagacagttatgtatgaac 736
QY 467 agatccaaagttacagagcttcttccacacacacacacacacacacacacacacacac 526
DB 737 agacccac 796
QY 527 acctccgaagaagaattgacacagttatgaagtgatcgtgacatcttccgtgacataa 586
DB 797 actgagagagagac 856
QY 587 aaagtgtgttctcaccac 646
DB 857 aaagtgtgttctcaccac 916
QY 647 taactgagac 706
DB 917 ccaagtcac 976
QY 707 tcaagaatgagtgctgctgacagatcttctccgaataatgacagatgacacacacacac 766
DB 977 tcaagaatgagtgctgctgacagatcttctccgaataatgacagatgacacacacacac 1036
QY 767 aattccccac 826
DB 1037 aattccccac 1096
QY 827 tattccgctgagatcaagttctcagttcagacacacacacacacacacacacacacacac 886
DB 1097 cattccgctgagatcaagttctcagttcagacacacacacacacacacacacacacacac 1156
QY 887 atactatgac 946
DB 1157 atactatgac 1216
QY 947 aaatccac 1006
DB 1217 aaatccac 1276
QY 1007 caacatgac 1066
DB 1277 ctac 1336
QY 1067 ttttgaagatgaagtaataagaatctgttccatgctggagagacacacacacacacacac 1126

DB 1337 gttgcaaatatgac 1396
QY 1127 aaactttatgagatgac 1186
DB 1397 aaactttatgagatgac 1456
QY 1187 taaagctgaagatgagatgac 1246
DB 1457 taaagctgaagatgagatgac 1516
QY 1247 taatcagttgagatgagatgac 1306
DB 1517 taatcagttgagatgagatgac 1576
QY 1307 accacggggtac 1366
DB 1577 accacggggtac 1636
QY 1367 tctaaagttctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1426
DB 1637 tctaaagttctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1696
QY 1427 cagatttgaagatgagatgac 1486
DB 1697 cagatttgaagatgagatgac 1756
QY 1487 cggac 1546
DB 1757 cggac 1816
QY 1547 gctgttgaatgagatgagatgac 1606
DB 1817 gctgttgaatgagatgagatgac 1876
QY 1607 tagtgagatgagatgagatgac 1666
DB 1877 tagtgagatgagatgagatgac 1936
QY 1667 tctcacaatgagatgagatgac 1726
DB 1937 tctcacaatgagatgagatgac 1996
QY 1727 gaaatgagatgagatgagatgac 1786
DB 1997 gaaatgagatgagatgagatgac 2056
QY 1787 ttatgctgaagatgagatgagatgac 1846
DB 2057 ttatgctgaagatgagatgagatgac 2116
QY 1847 ggaacagatgagatgagatgagatgac 1906
DB 2117 ggaacagatgagatgagatgagatgac 2176
QY 1907 tggatgagatgagatgagatgagatgac 1966
DB 2177 tggatgagatgagatgagatgagatgac 2236
QY 1967 ttgagatgagatgagatgagatgagatgac 2026
DB 2237 ttgagatgagatgagatgagatgagatgac 2296
QY 2027 tctacatctccac 2086
DB 2297 tctacatctccac 2356
QY 2087 gctgagatgagatgagatgagatgagatgac 2146
DB 2357 gctgagatgagatgagatgagatgagatgac 2416
QY 2147 tcaagcaatgagatgagatgagatgagatgac 2206
DB 2417 tcaagcaatgagatgagatgagatgagatgac 2476

```

QY 2207 atcaggaagatgaagagatcagatcattgtctcagagaaggaacccgttttgc 2266
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2477 atcaggaagatgaagagatcagatcattgtctcagagaaggaacccgttttgc 2536
QY 2267 atcatttctcagatcagatcagatcattgtctcagagaaggaacccgttttgc 2326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2537 ctttaatttctcagatcagatcagatcattgtctcagagaaggaacccgttttgc 2596
QY 2327 aagaacacagatcagatcagatcattgtctcagagaaggaacccgttttgc 2386
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2597 aagaacacagatcagatcagatcattgtctcagagaaggaacccgttttgc 2656
QY 2387 tcatgagagacagatcagatcattgtctcagagaaggaacccgttttgc 2446
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2657 tcatgagagacagatcagatcattgtctcagagaaggaacccgttttgc 2716
QY 2447 ggtgtacacacatgtagacagcagtggtctcagagaaggaacccgttttgc 2506
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2717 ggtgtacacacatgtagacagcagtggtctcagagaaggaacccgttttgc 2776
QY 2507 tgaattgagacatgtagacagcagtggtctcagagaaggaacccgttttgc 2550
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2777 agagaagaagtagacagcagtggtctcagagaaggaacccgttttgc 2820

```

RESULT 2

US-08-941-445A-14

Sequence 14, Application US/08941445A

Patent No. 6107060

GENERAL INFORMATION:

APPLICANT: Keeling, Peter

APPLICANT: Guan, Hanping

TITLE OF INVENTION: Starch Encapsulation

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P. C.

STREET: 5370 Manhattan Circle

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/941.445A

FILING DATE: 30-SEP-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/026,855

FILING DATE: 30-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Winner, Ellen P

REGISTRATION NUMBER: 28,547

REFERENCE/DOCKET NUMBER: 89-97

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 2725 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: mRNA

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Zea mays

FEATURE:

NAME/KEY: sig_peptide

```

; LOCATION: 91..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..2487
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..2490
US-08-941-445A-14

```

```

Query Match 43.0%; Score 1251.8; DB 3; Length 2725;
Best Local Similarity 75.4%; Pred. No. 0;
Matches 1556; Conservative 0; Mismatches 507; Indels 0; Gaps 0;

```

```

QY 430 ttctccacccggagaggaagaatataatgcatagatccagcttgcagcttgc 489
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 425 tccccccacacagcagatgagcaaaaatattccagattgaccccatgttccagcctata 484
QY 490 gtcacacatgattacacgattcagatcagacaaagacccggaagaaattgacagtc 549
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 485 agtacacatcttgactatgacgacgacgacgacgacgacgacgacgacgacgacgac 544
QY 550 atgaagtagtctgagatcattctctgctatgaaagattggttctcagcagtc 609
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 545 atgaagtagtctgagatcattctctgctatgaaagattggttctcagcagtc 604
QY 610 aacaggaataactatagagagtgagcaccagagagtcagtggtcgtcattgagag 669
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 605 cgaagagatgacatgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 664
QY 670 attcaataactggaatccatgacagatgacagatgacagatgacagatgacagatgacagat 729
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 665 acgtcacacacacacacacacacacacacacacacacacacacacacacacacacacacac 724
QY 730 agatccttgcggaataatgagagatgacacacacacacacacacacacacacacacacac 789
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 725 aaatttttctgcttgcacacacacacacacacacacacacacacacacacacacacacac 784
QY 790 agatgacatgacatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 849
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 785 agtgacatgacatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 844
QY 850 caattcaagcagcagatgacatcctcctcctcctcctcctcctcctcctcctcctcctcctc 909
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 845 cagtgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 904
QY 910 agaagtagtctgaaataatcctcctcctcctcctcctcctcctcctcctcctcctcctcct 969
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 905 taaagtatgcttgcacacacacacacacacacacacacacacacacacacacacacacac 964
QY 970 cgcacgttgaatgagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1029
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 965 cactgttcggaatgagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1024
QY 1030 atgtcttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1089
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1025 aagtcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1084
QY 1090 agcatcatattatgctcagcttgggtatcagtcacacacacacacacacacacacacacac 1149
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1085 agcactcatattatgagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1144
QY 1150 gatttgaacccctcagatgatttgaagcctcctaataagatcagcagcagcagcagcagc 1209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1145 gttttggtaccccgagagatgagccttggattgattgattgattgattgattgattgattgatt 1204
QY 1210 ttgtctcagatattgttcatagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1205 tagtttcacagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1264
QY 1270 tgttgatgtagcagatgtagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1329
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1265 gttttgattgtagcagatgtagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1324

```


QY	1937	tattaccatggaattgaacggaagaagatatttgaaatttagggaaatgaatttggaca	1996
Db	1201	tgtataccatggaatttgagagagaagggaactctaatttcaatgggaatgaattccgcca	1260
QY	1997	cccccgatggaattgattttccaaagaggtgatactacatacttcccaatgglaaatttgcttc	2056
Db	1261	ccccgatggaattgattttccctctagggctgacaacaacacctctctgattgctcgaattcc	1320
QY	2057	tgggaacaatltcaagttaagataaataatgcccgcgttaggtttgattctaagcaattccaagca	2116
Db	1321	cgggaaccaaatcaagttaatgataataatgcagacgaggaatttgacctgagatgacagataa	1380
QY	2117	tctgagatcatcat	2129
Db	1381	tttaagaataccgt	1393

```

1      RESULT 4
2      US-08-941-445A-16
3      ; Sequence 16, Application US/08941445A
4      ; Patent No. 6107060
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Keeling, Peter
7      ; APPLICANT: Guan, Hanning
8      ; TITLE OF INVENTION: Search Encapsulation
9      ; NUMBER OF SEQUENCES: 37
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESS: Greenlee, Winner and Sullivan, P.C.
12     ; STREET: 5370 Manhattan Circle
13     ; CITY: Boulder
14     ; STATE: CO
15     ; COUNTRY: US
16     ; ZIP: 80303
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: Floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/941,445A
24     ; FILING DATE: 30-SEP-1997
25     ; CLASSIFICATION: 800
26     ; PRIOR APPLICATION DATA:
27     ; APPLICATION NUMBER: US 60/026,855
28     ; FILING DATE: 30-SEP-1996
29     ; ATTORNEY/AGENT INFORMATION:
30     ; NAME: Winner, Ellen P
31     ; REGISTRATION NUMBER: 28,547
32     ; REFERENCE/DOCKET NUMBER: 89-97
33     ; TELECOMMUNICATION INFORMATION:
34     ; TELEPHONE: (303) 499-8080
35     ; TELEFAX: (303) 499-8089
36     ; INFORMATION FOR SEQ ID NO: 16:
37     ; SEQUENCE CHARACTERISTICS:
38     ; LENGTH: 2763 base pairs
39     ; TYPE: nucleic acid
40     ; STRANDEDNESS: single
41     ; TOPOLOGY: not relevant
42     ; MOLECULE TYPE: mRNA
43     ; HYPOTHETICAL: NO
44     ; ORIGINAL SOURCE:
45     ; ORGANISM: Zea mays
46     ; FEATURE:
47     ; NAME/KEY: transit_peptide
48     ; LOCATION: 2..190
49     ; FEATURE:
50     ; NAME/KEY: mat_peptide
51     ; LOCATION: 191..2467
52     ; FEATURE:
53     ; NAME/KEY: CDS
54     ; LOCATION: 2..2470
55     ; US-08-941-445A-16

```


QY	600	tcacgcagctgaaacacggaataactatagagatgaggcaccaggaagctagctgagctgca	659
Db	479	AACAGGGAAAGATGGTTGGCACTACTATCTGTAATGGCTCTCGTGGCTCCAGGAACGA	538
QY	660	ttgatctggagattcaataaactcggaalccctaaatgcagatgltcatgactcagaatgagtg	719
Db	539	GTTATTATGGGAAATTTCAATGGATGGAAAGCGTTCTTAACCATGATGAGGAGGACAGTTT	598
QY	720	gagctctggagatccttttggccgaataatgcagatgltcatcccaaatlcccatggt	779
Db	599	GGGTTTGGAGTATTAGATTCC---TATGTTCACGTAAAGCCAGTCATTCACACAAAC	655
QY	780	tctcgaaataaagatacgy---catgatatactcactctgcgaacaagaattatctctgct	836
Db	656	TCAGAGTTAAATGTTTCGTTTCAACATGTAATGGATGTGGTAAAGTCATACCTGGCT	715
QY	837	tgatataagatctcactgctcaag-----caccaggtgaactcccatataatgcatatac	890
Db	716	TGGATTAATATATGACCACTGCAGAGCCACCAAAAGTTTCACACACCATATGATGGTGTCTAC	775
QY	891	tatgatccctcccgagagagagaatgagtgtgtcaaaaactcctcagcccaagagaccaaa	950
Db	776	TGGGAACCCACACCTTCAGAAAGGTACACTTCAAAATACCTCGCCCTCCCAAAACCCGA	835
QY	951	tcactctgattatlgagtcgcacglttggaatgagtagtaagagagccagtaataacaa	1011
Db	836	GCCCCACGACATCTCAGAGCACATGTGGCATGTAGCGAGCTCTGAGCCACAGTAAATTCG	895
QY	1011	tatgcacaacttlaagagatgagtgtctctcgcatacaaaaagcttggctataatggtgt	1077
Db	896	TATCGTGAATTTGGCAGATGATGCTTTTACCTCGGATTTAAGCAAAATACATTAATATCTGTC	955
QY	1071	cagctcatggtcattcaagagacatcaatataatgctagtgttgggtatacgtlcaaac	1130
Db	956	CAGTTGATGGCCATTAATGGAACATTTCTTACTATGATGATCATTTGGATATCATGTTTCAACAC	1012
QY	1131	tttatagcagctagaagacggaattgggaacctgagatgattaaagctcttaatagataa	1199
Db	1016	TTTTTTCGTGAGCAATAGATATGGAACCCGGAGACCTTAAGATATCTGATAGATAA	1075
QY	1191	gtctacgagattaggtctctctgtctcctaigtatattgtlcatagacgatcatcaactaa	1250
Db	1076	GCACATACCTTGGGTTTACAGAGTCTGTGGATGTAGTTTCCACAGTCATCCAGCAATATAT	1133
QY	1251	acgttgagtgaggctggaatatgtttgat-----gftacggatggtlcaactacttcaac	1301
Db	1136	GTCACATGATGSCCTCAATAGCGTTTGGATTAATGGCCAAAGGTTCTCAAAATCATCACTTTTAT	1195
QY	1302	tctgagcaacggggatcatcatgactgagtctggagctctgcgccttttcaactatggggcg	1361
Db	1196	GCTGAGAGCGAGGGTACCATTAAGTGTGGGATAGCAGAGCTGTTCACATCTCCCAATTGG	1255
QY	1362	gaggttctaaagttctctcttccaaatlgcaagggtggtgtgtlgtlgtatgagtaagaattgat	1421
Db	1256	GAGGTCTTCCTTTCCCTTTCTTCCAACTTGAGGTGGTGGCTGTGAAGAGATATCACTTTGAC	1315
QY	1422	gggttccagatttgaatggggagacttcaaatgatacccatcatgagtttgaggtgat	1481
Db	1316	GGATTTGCATTTTGAATGGAATTAACCTTCATCTCTGTATATGTTTCATCATATGGAAATCAATATGGGA	1375
QY	1482	tttaccggcaactacaalgaataactttggtatgalybaacactgagtatgagtgtgtttat	1541
Db	1376	TTTTCAGGAACCATATATATGTGATATTTTCAGGAGGCTACAGATGTTGATGTGTGGTAT	1435
QY	1542	ttgatgctggttgaatgataatgataatgcttgctctccagagcgctgataccattggtgaa	1601
Db	1436	TTAATGTTGGCCAAATATATCTGATTTCCAAAGATTTTCCAGAGCAACGTTATTTGCCGAA	1495
QY	1602	gagtttagtgaatgccacaagattttgcatctccggttgaagaatgagtgtgtgttgctgat	1661
Db	1496	GATGTTTCTGTATGCGCGGCGCTTACCGGCGCGTTTCTTGAGAGGAGAAATTGTTTTGAT	1555


```

Db      476  TCCAGAGTAAAGTTGCTTCCAAACATGATGATGAGTGTGGGTACATGCTTCCTGCT 535
Qy      837  tggatcaagttctcaagttcaag-----caacagtgtaactcccatataatgagcatatc 890
Db      536  TGGATAAAGATGACCATGACGACGCCACAAAGTTGACAGACCATATGATGTGTCTAC 595
Qy      891  tatatctcccgagagagagagatgtgtgtcaaaaaccccaagcaagagaccacaa 950
Db      596  TGGAGCCACCATCTTACAGAAAGTACCACTTAAATACCTGCGCTCCCAACCCCA 655
Qy      951  tcaacttggaattatgaagtcacgttgaatgaagtagtagcagagccaagtaataca 1010
Db      656  GCCCCACAGATCTACGACGACATGTGCGATGACGAGCGTACGACAGCTGAATATCG 715
Qy      1011  taagcaacttagagatgagtgctctcgatcaaaaagcttggtacaagtcgt 1070
Db      716  TATCGTAGTTTCCAGATGATGTTTACCTCGATTAAGCAAAATATATATATCTGTC 775
Qy      1071  cagctcatgctatcaagaagcatcatatatagtctagtttggttatcacgtcaaac 1130
Db      776  CAGTTGATGCGCATATATGAGACATTTCTATGATCATTTTGATATCATGTTATCAAC 835
Qy      1131  tttaagcagctagaagccagatttgaaactcctgatatlaaagltcctatagataa 1190
Db      836  TTTTGTGCTGTGACAAATGATGAAACCCGAGAGACCTTAAGTATCTGTATGATMAA 895
Qy      1191  gccacagatgaagttcttctcagatgatatgtttcaagcagcatcaactaat 1250
Db      896  GCACATAGCTTGAGTTTACAGGTTTGTGATGTGATGATGATGATGATGATGATGAT 955
Qy      1251  aagttgagtgagtgatgatttgat-----ggtacagatgagtcactacttcaac 1301
Db      956  GTCACTAGTGCGCTCAATGCTTGTATTTGCGCAAGTGTCTCAAGATTCCTACTTCTAT 1015
Qy      1302  tctgagccaggggtatcatattgagtgagagctctcgctttcaactatggagctgg 1361
Db      1016  GCTGGAGAGCGAGGATACCATAGTTGTGGATGACAGGCTTCTCAACTATGCCAATTTG 1075
Qy      1362  gaagttcaagttcttcttcaaatgcaagtggtgtgtgtgtgtgtgtgtgtgtgtgt 1421
Db      1076  GAGGTTCTGCTTCTCTCTCTTCCAACTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGT 1135
Qy      1422  ggggtcagaattgagtgagtgatcaatgatatgatacccaatcagtgatgagtgat 1481
Db      1136  GGATTTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1195
Qy      1482  tttaacggaaactacaagaactttgatatgataagctgtatgagtgatgagtgat 1541
Db      1196  TTTTACGGAATCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1255
Qy      1542  ttgagctgttgaatgatatgatatgatatgctctcccaagagtggttcaacatgagaa 1601
Db      1256  TTAATGTTGGCCAAATATCTGATTCACAAAGATTTTCCAGACGCACTGTTATTTGCCG 1315
Qy      1602  gattgttagtgaagtcacaagatttgatcccggttgaagaatggtgtgtgtgtgtgt 1661
Db      1316  GATGTTTCTGTATGCTCGGGGCTTAGCGGCTTCTGTGAGGAGGAATTTGTTGAT 1375
Qy      1662  tatcgtccacatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1718
Db      1376  TACGCGCTGGCAATGCAATCCCAATATGATGATGATGATGATGATGATGATGATGATG 1435
Qy      1719  gaagaatggaatggtgtgacattgtatataatgctgaacacagcggtgtgtgtgtgt 1778
Db      1436  GAAAGTTGCTCCATGAAAGAGTAAATCGATTTGACAAATAGGAATATACAGAGAG 1495
Qy      1779  tgtgtcttctgtcgaagtcagtcagcagcctgtgtgtgtgtgtgtgtgtgtgtgtgt 1838
Db      1496  TGTATAGATATGTCGGAAGACATGATGATGATGATGATGATGATGATGATGATGATG 1555
Qy      1839  tggctatggaacaggaatgatatgacttgcgtcttgacagacacatctactctc 1898

```

```

Db      1556  CTCCTAATGAAACAAAGATATTTCTGGCANGCTTGTGCTGACAGATGCTTCTCTGTT 1615
Qy      1899  atagatcgtgagtagatgagtcacaaatgat-cagagcttataccatgagtgagtg 1957
Db      1616  GTTATGACGAGATTTGGCTTGTGACAAATGATATCAATTTTTCACAAATGCTTGGAGG 1675
Qy      1958  agaagatattgaattttagtgaatgaatgtgacaccccgagtgatgatttcc 2017
Db      1676  AGAGGGGTACCTCAATTTCAATGGGTAAACGATTTGGCCATCTCGATGATGATGATG 1735
Qy      2018  aagagtgatcatcatcttccagtggttaatttctcgttggaacaaatlaagatga 2077
Db      1736  TAGTGAG-----GGCAATTAATGAGATTAAGA 1762
Qy      2078  taagtccggtgagttgagatgaagcaatcaagacatcagagatcagatgaatga 2137
Db      1763  CAATGTAAGCGCAGTGGACCTGCAATAGCAGACACTGATATCAAGTTATATGA 1822
Qy      2138  agagtttgatcaagcaatcagacatctgaagaagcctatggtttcagactctga 2197
Db      1823  TGCATTTGATGAGCTATGAAATTCGCTCGATGAAAGTTTCATTCCTCGCATGAGAA 1882
Qy      2198  ccaatcatacacggaagatgaagagatgagatgagatcttctcagagaggaaact 2257
Db      1883  ACAGATAGTATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1942
Qy      2258  cgttttgatcaatattcatttgagtagcagacttgcagatccagagtgagtgct 2317
Db      1943  GGTATTTGATTTCACTTCCACCAATATACATACAGGATTAAGTTGATGATGATG 2002
Qy      2318  aaagcaggaagaatgaatgaatgagtgatcagatcagatccttctgttgagagct 2377
Db      2003  CTGCGAGGAGATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2062
Qy      2378  cagagtgatcagatgagtcagacactca 2406
Db      2063  AAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2091

```

```

RESULT 7
US-08-981-803-29
; Sequence 29, Application US/08981803
; Patent No. 6147279
; GENERAL INFORMATION:
; APPLICANT: ROUSEN, PETER
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2004
; CURRENT APPLICATION NUMBER: US/08/981,803
; EARLIER FILING DATE: 1997-04-17
; EARLIER APPLICATION NUMBER: PCT/EP96/03052
; EARLIER FILING DATE: 1996-07-12
; EARLIER APPLICATION NUMBER: 9514435.8
; EARLIER FILING DATE: 1995-07-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11478
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-981-803-29

```

```

Query Match      12.7%; Score 369; DB 3; Length 11478;
Best Local Similarity 64.3%; Pred. NO. 8.5e-103;
Matches 590; Conservative 0; Mismatches 315; Indels 12; Gaps 2;

Qy      910  agaagatgltgtcaaaaatctcagccaagagacccaatctcagattatgagt 969
Db      5242  acaagttaccacttaataaacctgcctcccaaaccccgagcccaagaatatagaag 5301
Qy      970  cgcacgttggaatgagtagtcagagccagatataacatatgccaacttagagatg 1029
Db      5302  cacatgtcgcagtagcagcgtctgagccacgtgttaattcgtgtgtgtgtgtgtgt 5361

```



```

OY 1030 atgtgctctccgcatcaaaaagcttggtctacatgctgctcagctcgtatcgaag 1089
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5362 atgttctcccgagtaagcaataactatatactcgtccagttagtgagcgaatg 5421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1090 agcatctattatgctggtttgtgtatcacgtccaaactttatgagctgagcggc 1149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5422 aacattcttaactatgagatcatgtgatactgttacaactttttgtgtgtagcgta 5481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1150 gatttgaaactcgtgatttaaaagctcctaataagataaaagcccaagagtaagcttc 1209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5482 gataagaaacccgaggaacccaagatccgataagaaagcaatagccttggtttac 5541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1210 ttgtctcaatgagataatgttcaatagcaatcaactaactagcttgatgagctgaata 1269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5542 aggtctgtgtgtatgtatgtacagctacgaagcaataatgtaactgataagcctcaatg 5601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1270 tgtttgat-----gtaacgagatgttcaactcttcaactctgagacaggggtcaatc 1320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5602 gctttgataatgtgcgaaggtttctcaagaatccctacttcaatgtctgaaagcgaaggtacc 5661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1321 atgtgagtgaggaactcgcctttcaactatgagagctggagaggtttcctaagttcttc 1380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5662 ataagttggtgagatagcagagctgttcaactatgcaatgtgagaggtttctcgttcccttc 5721
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1381 ttccaagtcaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5722 ttccaacttgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1441 tgaactcaatgataagcaaccatctgagatgtagagatattacccgcaactacaatg 1500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5782 taactctatgtgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 5841
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1501 aatacttgatataagcaactgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 1560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5842 agtaattcagcagagcaatgaagatgtgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5901
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1561 tgaattcagtgctctcccaagagctgtcaacatgtgtgaaagatgtgtgtgtgtgtgtgtgtgt 1620
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5902 tgaattcagaagatcttcccaagagcaactgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5961
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1621 cagttgcatctccggttgaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5962 gacctgagcggcgtcttcttgagggaggaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6021
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1681 ttgctgataaattggtgtgagatbaltcaag---aagagagatgaaagatgtgaaatgtgtgt 1737
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6022 tcccaagataagtgagatagattatttaagaataaagatgataagatgtgtgtgtgtgtgtgtgt 6081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1738 acaattgacatatgtcagcaacagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1797
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6082 aagtaacatagagtttgcaaaatagagatatacagaagaagtgtatagacatgtcggagaa 6141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1798 gtcatgacagagccctt 1814
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6142 cccatgacaggtattt 6158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11478
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)-(11478)
; OTHER INFORMATION: B stands for G or C or T/U
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)-(11478)
; OTHER INFORMATION: R stands for G or A
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)-(11478)
; OTHER INFORMATION: K stands for G or T/U
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)-(11478)
; OTHER INFORMATION: W stands for A or T/U
; NAME/KEY: variation
; LOCATION: (1)-(11478)
; OTHER INFORMATION: M stands for A or C
; US-08-983-440-29

Query Match      12.7%; Score 369; DB 4; Length 11478;
Best Local Similarity 64.3%; Pred. No. 8.3e-103;
Matches 590; Conservative 0; Mismatches 315; Indels 12; Gaps 2;

OY 910 agaagatgtgttcaaaaatccctcgaagcaagagcaacaaatcaactcgtgattatgagt 969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5242 acaggtaccacttcaaaatccctcgtccctcccaaccccgagcccaagatctatgaag 5301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 970 cgcacgttgatagatgagtagcagagcaagtaattacaacatgtccaacttggagatg 1029
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5302 cacatgtcgatagagcagctcgtgacacgtgtgaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1030 atgtgctccctcgcatcaaaaagcttgctacaaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1089
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5362 atgttttaactcgtgattgaagcaataactataactgttcacgttgaatgtgtgtgtgtgtgtgtgt 5421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1090 agcatctattatgctgagttttgtgtatcaagctacacaaactttagacagcttagcagcc 1149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5422 aacattctactatgagatcatttggatatactgttacaactttttgtgtgtgtgtgtgtgtgtgtgt 5481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1150 gatttgagaccccgatgatttaagctctctaataagataagctcaagctgagctgtgtgtgtgtgtgtgt 1209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5482 gataagaaacccgagagagcaactaagatctgtatgataagcaacatagctgtgtgtgtgtgtgtgtgt 5541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1210 ttgtctcaatgataatgttcatagcagatgcatcaactaaactgaactgtgtgtgtgtgtgtgtgtgt 1269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5542 aggtctcgtgtgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1270 tgtttgat-----gtaacgagatgtcactcttccctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5602 gcttggataatgtgcgaaggtttctcaagaatccctacttcaatgtctgaaagcgaaggtacc 5661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1321 attgagtggtgagctcgcctttcaactatgagagctggagagctgtaaggtttcttc 1380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5662 ataagttgtgagatagcagcgtgttcaactatgcaactatggaaggtttcgtgtgtgtgtgtgtgtgt 5721
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1381 ttccaagtcaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5722 ttccaacttgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1441 tgaactcaatgataagcaaccatcaatgataatgtcagtgatatttaccggcaac--acaagt 1500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5782 taactctatgtgtatgttcaatcagatgaatcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5841
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1501 aatacttgagatgcaactgatagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


Db	5842	agatattcagcgagcggtactacagatggttgatgctgctgtctatttaagtgtgccaataatc	5901
Qy	1561	tgatatacgtctctctcccaagagctgtcacattggtggaagatgltagtgtgaatgccaa	1620
Db	5902	tgattccacaagatcttccccagagatgcacaactgtattgtccgaagatgttcttgatgcg	5961
Qy	1621	cagtttcgattccggtgttgaaagatggtgtgtgtgccttgattatcgcttcccaatgctg	1680
Db	5962	gccttgcgcggtcccggttctctgaaggaggaatggtgtgtttgttaacgcgcgcgaatgacaa	6021
Qy	1681	ttgtcgtataaattggtgtgagattattccag---aagagagatgaagatttggaatatggtgt	1737
Db	6022	tcccaagtaagtgtgataagattatttaagaataaagatgataagattgtgtccatgaag	6081
Qy	1738	acattgtacatatgctgacacacagcggtgtgttgaaagtgtgttcttatgtctgaa	1797
Db	6082	aagtaaacatcgagatttgacaaataagaagataacagagaagatgltataacatatgcgagaa	6141
Qy	1798	gtcatgacacggccctt	1814
Db	6142	cccaatgatacagatttt	6158

```

RESULT          9
US-08-528-026C-3
: Sequence 3, Application US/08528026C
: Patent No. 6248566
: GENERAL INFORMATION:
: APPLICANT: IMANAKA, Tadayuki
: APPLICANT: TERADA, Yoshinobu
: APPLICANT: TAKAHARA, Takeshi
: APPLICANT: YANASE, Michiyo
: APPLICANT: OKADA, Shigetaka
: APPLICANT: TAKATA, Hiroki
: APPLICANT: NAKAMURA, Hiroyasu
: APPLICANT: FUJII, Kazutoshi
: TITLE OF INVENTION: GLUCAN HAVING CYCLIC STRUCTURE AND METHOD FOR PRODUCING THE SAME
: FILE REFERENCE: 9900-0002..20
: CURRENT APPLICATION NUMBER: US/08/528.026C
: CURRENT FILING DATE: 1995-09-13
: PRIOR APPLICATION NUMBER: US 08/415,152
: PRIOR FILING DATE: 1995-03-31
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 2426
: TYPE: DNA
: ORGANISM: Bacillus stearothermophilus (Strain TBRE14)
: FEATURE:
: NAME/KEY: misc:feature
: LOCATION: (385)..(392)
: OTHER INFORMATION: S SD sequence
: NAME/KEY: misc:feature
: LOCATION: (402)..(2357)
: OTHER INFORMATION: P CDS
: US-08-528-026C-3

```

Query Match	2.3%	Score	68.4	DB 4	Length	2426
Best Local Similarity	48.5%	Pred. No.	8.3e-11			
Matches 220; Conservative	0	Mismatches	231		Indels	3
					Caps	1

QY	1003	ttaacatattatgccaacttttagatgtagtggcttctctcgatacaaaagaagctgtgtcaca	1065
Db	895	tttaaacgtaccagtcgaatgagccgatacgtatctctgtagtgcctgcatactgtgttta	954
QY	1063	atgctgttcagctcatatgctatcaaaagatcatcatatattctagtttggatcacg	1122
Db	955	cgcacattgattgtctctctctcgtctgcagatccgtctgcacgcgtctggaggctacaa	1014
QY	1123	tcacaactttatgcagctagcagccgattcttggaaactccgtatgtattaaagctctaa	1182

Db	1015	gaacagggtatlaagcgttaacagatgcgatcgtatggtacgcgaacagacttcaactgcttcg	1074
OY	1183	tagataagctcacagaggttagtgccttccttccttaagatatttttaacacatgat	1242
Db	1075	tcgaacggttcacatcagcgcggaatcgggtacattatgtaacatcggtgtccgggacatttt	1134
OY	1243	caactaatacgtttgatalcggcctgaatatgttttagatgtaacgatalgctcaacttcaact	1302
Db	1145	gcaaggagcgc---ccatagggtatataatgtttatgtgcgcccgacgtatgatatgcga	1191
OY	1303	cttgaccacacgggagatcatcttgatgtggtgacctgcgcttccttcaactatgtagagctgg	1362
Db	1192	atgaaaaagacacgggaataatcagcttctggggagcgcacatttgatttaaggcaacgcgg	1251
OY	1363	aggtctaaagttctcttccttccaatgcaaggtggtgtgttgatgtaagaatttgatg	1422
Db	1252	aagtgccaaagtttctcatatcgaacacatgtgttctggtcgaattaccatcacatcagcg	1311
OY	1423	ggttcagaattgtagtgggtgacttcaatgatga	1456
Db	1312	ggttcgcggtcgaatgcggttgccaatatgtttta	1345

```

US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKNER, P. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTgpt-F15

```

```

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Derived from plasmid pSF\1 (Agric. Biol. Chem.
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1404 /note= "Nucleotides 1-1404
OTHER INFORMATION: correspond to nucleotides 79-1482 in the Saccharomycopsis
OTHER INFORMATION: fibuligera `amylase structural gene"
US-08-204-656B-1

Query Match 1.4%; Score 41.4; DB 1; Length 1404;
Best Local Similarity 56.1%; Pred. NO. 0.012;
Matches 78; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 1100 ttatgcagatttgaggatcatcagtcacaacattatgcagctacagccagattggaac 1159
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 231 TTATGCTTATCATGAGTTCCTTGATGAGAACATATATCAAAATTAATGAGAACTTTGGTAC 290

Qy 1160 tccgcagatttlaaagctctctatagataaagctcagagattggtctctgttcacat 1219
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 291 TGCTGATGATTGAATGAATCTTTGGCACAAAGATTGCACGATCGTATATGTTGTAATAGT 350

Qy 1220 ggatattgtctacaagccat 1238
||||| ||||| ||||| ||||| |||||
Db 351 GGATATGTTACCAACCAT 369

RESULT 12
US-08-204-656B-3
Sequence 3, Application US/08204656B
Patent No. 5538882
GENERAL INFORMATION:
APPLICANT: Matsui, Ikuro
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyai, Sachio
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: 8110 Gatehouse Road, Suite 500 East
City: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/204,656B
APPLICATION NUMBER: US/08-MAR-1994
FILING DATE: 02-MAR-1994
CLASSIFICATION: A15
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:

```


Fri Aug 10 16:32:41 2001

us-09-297-703a-28.Aug9.rni

Page 14

REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-470-702-1

Query Match 1.4%; Score 41.4; DB 1; Length 1404;
Best Local Similarity 56.1%; Pred. No. 0.012; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 61;
QY 1100 ttatgctagtttgggtatcagtcacaaactttatgcaagtcagccgattgggaac 1159
DB 231 ttatgctatcattggtttggtatcagtcacaaactttatgcaagtcagccgattgggaac 290
QY 1160 tccctgatgatttaagtcctctaataagataagtcagagtagtcttcttcttccat 1219
DB 291 tgcctgatgatttgaagtcctctaataagataagtcagagtagtcttcttcttccat 350
QY 1220 ggaattgttcataagccat 1238
DB 351 ggaattgttcataagccat 369

RESULT 15
US-08-470-702-2
Sequence 2, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 810 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-470-702-2

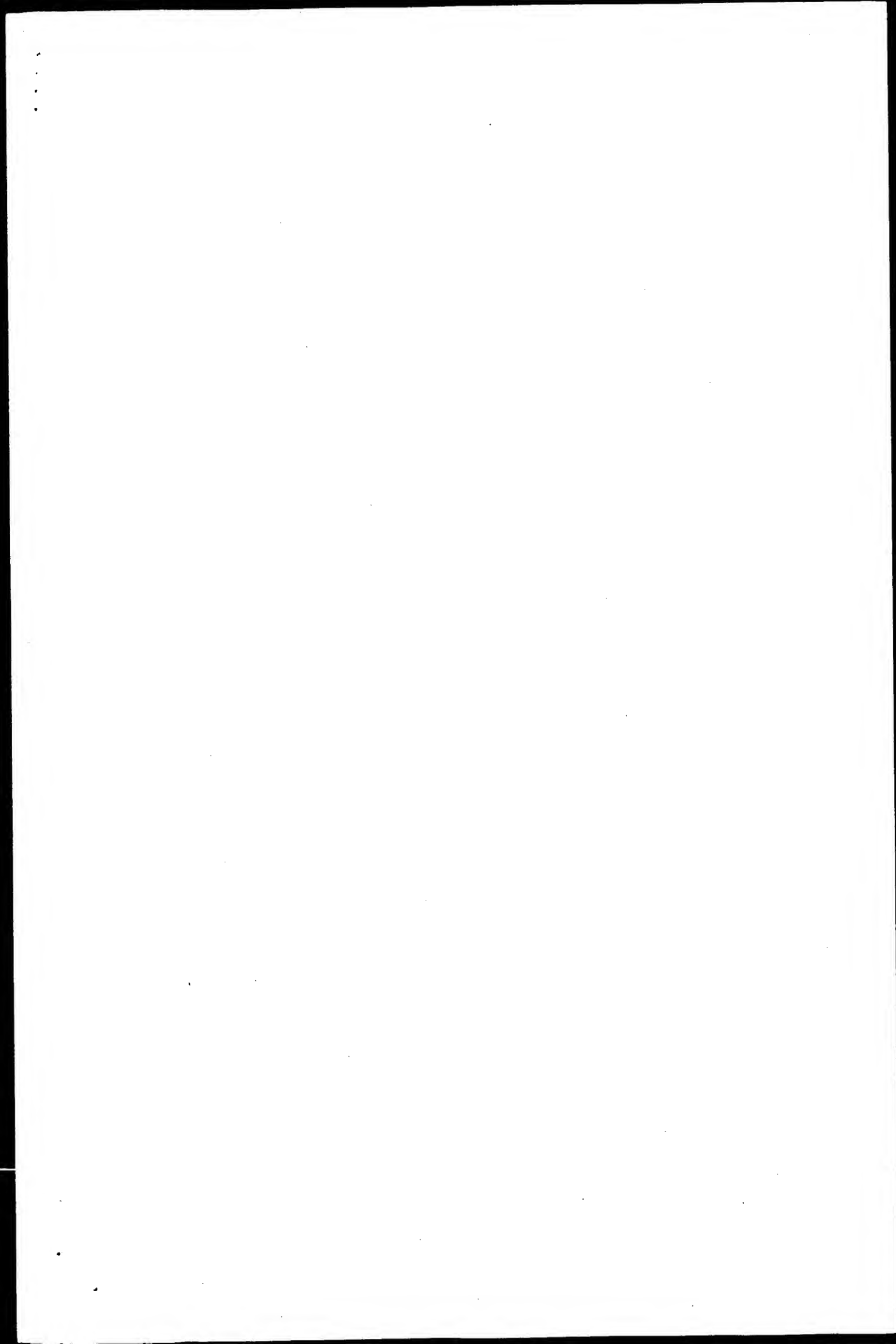
Query Match 1.4%; Score 41.4; DB 1; Length 1404;
Best Local Similarity 56.1%; Pred. No. 0.012; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 61;
QY 1100 ttatgctagtttgggtatcagtcacaaactttatgcaagtcagccgattgggaac 1159
DB 231 ttatgctatcattggtttggtatcagtcacaaactttatgcaagtcagccgattgggaac 290
QY 1160 tccctgatgatttaagtcctctaataagataagtcagagtagtcttcttcttccat 1219
DB 291 tgcctgatgatttgaagtcctctaataagataagtcagagtagtcttcttcttccat 350
QY 1220 ggaattgttcataagccat 1238
DB 351 ggaattgttcataagccat 369

Search completed: August 10, 2001, 12:49:44
Job time: 6506 sec

Fri Aug 10 16:32:41 2001

us-09-297-703a-28.Aug9.rni

Page 15



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2001, 10:33:13 ; Search time 3839.78 Seconds

(without alignments)

11734.410 Million cell updates/sec

Title: US-09-297-703a-28

Perfect score: 2913

Sequence: 1 ctcttaacttcagcgaa.....aaaacacacacacacacacatcgcg 2913

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_da1:*
- 2: gb_da2:*
- 3: gb_da3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_cm:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_pl1:*
- 13: gb_pl2:*
- 14: gb_pl3:*
- 15: gb_pl4:*
- 16: em_da1:*
- 17: em_da2:*
- 18: em_fun:*
- 19: em_hcgo_hum:*
- 20: em_hcgo_inv:*
- 21: em_hcgo_rod:*
- 22: em_hcgo_hum1:*
- 23: em_hcgo_hum2:*
- 24: em_hcgo_hum3:*
- 25: em_hcgo_hum4:*
- 26: em_hcgo_hum5:*
- 27: em_hcgo_hum6:*
- 28: em_hcgo_hum7:*
- 29: em_hcgo_hum8:*
- 30: em_hcgo_inv1:*
- 31: em_hcgo_inv2:*
- 32: em_hcgo_other:*
- 33: em_hcgo_rod:*
- 34: em_hum1:*
- 35: em_hum2:*
- 36: em_hum3:*
- 37: em_hum4:*
- 38: em_hum5:*
- 39: em_hum6:*
- 40: em_hum7:*
- 41: em_in:*
- 42: em_cm:*
- 43: em_or:*

44: em_ov:*

45: em_pat:*

46: em_ph:*

47: em_pl:*

48: em_ro:*

49: em_sts:*

50: em_sy:*

51: em_un:*

52: em_v1:*

53: gb_sts1:*

54: gb_sts2:*

55: gb_sts3:*

56: gb_sy:*

57: gb_un:*

58: gb_v11:*

59: gb_v12:*

60: gb_hg1:*

61: gb_hg2:*

62: gb_hg3:*

63: gb_hg4:*

64: gb_hg5:*

65: gb_hg6:*

66: gb_hg7:*

67: gb_hg8:*

68: gb_hg9:*

69: gb_hg10:*

70: gb_hg11:*

71: gb_hg12:*

72: gb_hg13:*

73: gb_hg14:*

74: gb_hg15:*

75: gb_hg16:*

76: gb_hg17:*

77: gb_hg18:*

78: gb_hg19:*

79: gb_hg20:*

80: gb_hg21:*

81: gb_hg22:*

82: gb_hg23:*

83: gb_hg24:*

84: gb_hg25:*

85: gb_pr1:*

86: gb_pr2:*

87: gb_pr3:*

88: gb_pr4:*

89: gb_pr5:*

90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

94: gb_pr1:*

95: gb_pr2:*

96: gb_pr3:*

97: gb_pr4:*

98: em_da3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2913	100.0	2913	9 A92162	A92162 Sequence 28
2	2028	69.6	3090	9 A92164	A92164 Sequence 30
3	1475.2	50.6	3549	14 PSSBEIGEN	X80009 P.sativum m
4	1467.4	50.4	3360	12 AB029548	AB029548 Phaseolus
5	1396.4	47.9	2517	12 AB042937	AB042937 Ipomoea b
6	1392.4	47.8	2542	14 ATU22428	U22428 Arabidopsis
7	1384.8	47.5	2493	15 STSBEIT	AJ000004 Solanum t
8	1382.8	47.5	2523	15 STU01889	AJ01889 Solanum t

[illegible]

```

Db      841 TCAGATTCACGTCACACAGGTGAACCCATTAATGATATGATATCTC 900
OY      901 CGAAGAGAGAGAGATATGTCCTCAAAATCCTCAGCAAGAGCAAAATCCTCAG 960
Db      901 CGAAGAGAGAGAGATATGTCCTCAAAATCCTCAGCAAGAGCAAAATCCTCAG 960
OY      961 ttatagatcgacgcttggaatgagtagtaacgagcaagtaataacatatacgcaac 1020
Db      961 TTTATGATCGACAGTTCGATGAGTACGAGCCAGATTAACATATGAGCCAACT 1020
OY      1021 tttagatgtagtgccttcctgcacatacaaaagcttggctacaatgctgctcagctatg 1080
Db      1021 TTAGAGATGATGTCCTTCCTCGCATCAAAAAGCTTGCTCAATGCTGTCACATGAG 1080
OY      1081 ctatcaagagcattcatatattatgctagtttgggtatcgcgtcaacaactttatgca 1140
Db      1081 CTATTCAGAGACATTCATATATATGCTATGTTGGTATACGTCACAAACTTTATGCA 1140
OY      1141 ctgacagcgatcttggaactcctgtagtattlaaagctctcaatagaataagctcagagt 1200
Db      1141 CTACAGCCGATTTGGAACCTCGATGATTTAAAGTCTCAATAGATTAAGCTCACGAGT 1200
OY      1201 tagtctcttctgctcatatgatatattgttcaatagcattcaactaataacgttagatg 1260
Db      1201 TAGCTCTCTTCTGTCATGATGATGTTGTTCAATGAGCCATGATCACTAATAGCTTGATG 1260
OY      1261 ggcctgaatgatttgaatgtagtgcacacacacacacacacacacacacacacacacac 1320
Db      1261 GGCTGATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
OY      1321 attgagatgtagtgccttccttcacactaagagagctggaagcttcaagcttctc 1380
Db      1321 ATTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
OY      1381 ttcaaatgcaagctgtagtgcacacacacacacacacacacacacacacacacacacac 1440
Db      1381 TTTCAATGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
OY      1441 tgaactcaatgtagtgcacacacacacacacacacacacacacacacacacacacacac 1500
Db      1441 TGACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
OY      1501 aactccttgatagtagtaactgtagtgccttcaactaagagagctggaagcttcaagctt 1560
Db      1501 AATACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
OY      1561 tgaactcaatgtagtgcacacacacacacacacacacacacacacacacacacacacac 1620
Db      1561 TGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
OY      1621 cagttgcatcctcggttggaagctgtagtgccttcaactaagagagctggaagcttcaag 1680
Db      1621 CAGTTGCACTCGGTTGGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1680
OY      1681 ttgctgataaattggttgtagatattcaagaagaagatggaagattggaattggaattgga 1740
Db      1681 TTGCTGATTAATGGGTTGATGATTAATCAAGAGAGATGAAAGATGGGTTGACA 1740
OY      1741 ttgtacatactgtagcaacacagcggtggttggaagctggttcttcaatgcttcaagct 1800
Db      1741 TTGTATCATATGCTGACCAACAGCGGTGTTGAAAGATGCTGTTTATGCTGAAGTGC 1800
OY      1801 atgacacagcccttggttgtagcaaaactattgcttggctgtagtgcacacagatattg 1860
Db      1801 ATGACACAGCCCTTGTGTGTGACAAATATTTGCTATGCTATGCTATGCTATGCTATGCT 1860
OY      1861 atgacttcatgctctgtagacacacacacacacacacacacacacacacacacacacac 1920
Db      1861 ATGACTTCATGCTCTGACAGACACATCTACTCTCTCATAGATCGTGGAGTACATGCT 1920
OY      1921 aaaaaatagaagcttatacctatgtagtgaagcggaagaagatttcaattatgag 1980

```

```

Db      1921 ACAAATGATCAGGCTTATTCATGAGATTAGCGGAGAGAGATATTGATTTATG 1980
OY      1981 gaaatgaatttggagaccccgagtgtagtatttccaagaagtgatcatcatcttcca 2040
Db      1981 GAAATGAATTTGGACACCCCGAGTGATGATTTTCCAAAGAGGATCTCATCTTCCCA 2040
OY      2041 gtgttaaatcttctccttgtagacacacacacacacacacacacacacacacacacacac 2100
Db      2041 GTGTAATTTGTTCTCTGAGAACAAATTCAGTATGATTAATCCCGCGTAGGTTGATC 2100
OY      2101 taggaatctaaagcatctgtagatatacgtgaatgcaagagcttgaatgaacacacac 2160
Db      2101 TAGGCAATTCAAACATCTGAGATATCATGGAATGCAAGAGTTGATCAAGCAATTCAC 2160
OY      2161 atctgaaagacacacacacacacacacacacacacacacacacacacacacacacacac 2220
Db      2161 ATCTTGAAGAAGCCTATGCTTTCATGCTCTGAGCAACCAATTCATATCCGAGAGATG 2220
OY      2221 aaagagatcgatcatctgctcctcgaagaggaacacacacacacacacacacacacac 2280
Db      2221 AAAGGATCGGATCATCTGCTGAGAGGAGAAACCTCGTTTGTATTCATTTTCAT 2280
OY      2281 ggaactagacacacacacacacacacacacacacacacacacacacacacacacacacac 2340
Db      2281 GGACTACACGCTATTCGATTCAGAGATGAGAGTGGCTGTTAAAGCAGAGAAATCAAGATG 2340
OY      2341 tcttgatcaatgtagtgccttcttggaagcttctgcaagcttctgcaagcttctgcaag 2400
Db      2341 TCTTGTGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
OY      2401 acttgaagcttgaagagtgtagtgcacacacacacacacacacacacacacacacacacac 2460
Db      2401 ACTTTCACCTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460
OY      2461 gtagaagcagtgtagtgcacacacacacacacacacacacacacacacacacacacacac 2520
Db      2461 GTAGAACAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
OY      2521 tgcgaggttaagatatacttcaacacacacacacacacacacacacacacacacacacac 2580
Db      2521 TCGCCGTTAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
OY      2581 cctatgtaactgtagtgcacacacacacacacacacacacacacacacacacacacacac 2640
Db      2581 CCTATGATCATCTGCTTAAAGCAATATATGATGATGATGATGATGATGATGATGATGATG 2640
OY      2641 gcaagatcttccatcctgtagtgcacacacacacacacacacacacacacacacacacac 2700
Db      2641 GCAGATTTCCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
OY      2701 taggaagcagaggttaagtagtgcacacacacacacacacacacacacacacacacacac 2760
Db      2701 TAGGAAGCCAGGTTTACATGCTTCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2760
OY      2761 calaaacttcaagctgtagtgcacacacacacacacacacacacacacacacacacacac 2820
Db      2761 CATTAATCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
OY      2821 ttatcatgtagtgcacacacacacacacacacacacacacacacacacacacacacacac 2880
Db      2821 TTATCATGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880
OY      2881 taagtttaaaaaaaacacacacacacacacacacacacacacacacacacacacacac 2940
Db      2881 TAAGTTTAAAAAAAACCAAAATATCCATG 2940

```

RESULT 2
 A92164
 LOCUS A92164 3090 bp DNA
 DEFINITION Sequence 30 from Patent WO9820145.
 ACCESSION A92164
 VERSION A92164.1 GI:6740960

[illegible]

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
5800009.1	GI:510545	SBEI gene; starch branching enzyme I.	pea.											
			<i>Plum sativum</i>											
			Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta											
			Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;											
			Fabales; Fabaceae; Papilionoideae; Plum.											
			1 (bases 1 to 3549)											
			Burton, R.A., Bewley, J.D., Smith, A.M., Bhattacharya, M.K., Tatge, H.,											
			Ring, S., Bull, V., Hamilton, W.D. and Martin, C.											
			Starch branching enzymes belonging to distinct enzyme families are											
			differentially expressed during pea embryo development											
			Plant J. 7 (1), 3-15 (1995)											
			95201826											
			2 (bases 1 to 3549)											
			Burton, R.A.											
			Direct Submission											
			Submitted (01-JUL-1994) R.A. Burton, John Innes Institute, Colney											
			Lane, Norwich NR4 7UH, UK											
			Location/Qualifiers											
			1..3549											
			/organism="Plum sativum"											
			/db_xref="taxon:3888"											
			/dev_stage="embryo"											
			/clone_lib="CDNA LAMBDA gt11"											
			/cell_line="JI:430 BCI9BR"											
			220..363											
			/gene="SBEI"											
			220..2988											
			/gene="SBEI"											
			/codon_start=-1											
			/product="starch branching enzyme I"											
			/protein_id="CAA56319.1"											
			/db_xref="GI:1345570"											
			/db_xref="SPTREMBL:Q41058"											
			/translation="MYVTISIRRPVPLPSLHKSNTKCRDPPASHPSELKNNSSSRP											
			SLYAKSRSEKSTSTIAESDKYLIPEDDONSVLADQLENDPTISEDNQLEDTIMK											
			DKGKYVIDESTSYREVDKGVSTSSLDVNTIDQAKTSVHSDKRVKDKPIL											
			PETGKRTIETDPLQAHQHLDFRYGYKRIIEELIDYKEGLIDFANADGSPILPHG											
			AGTIVREMAPGAKSAALVGDPMNPNADVMKDAFGWELFLPNADGSPILPHG											
			RYAIHNDTPSGIKDSIPIMAKIFESVOADGELIPYNGIYDDPEEKVYFHPDKRPOS											
			RIYSHIIGMSPEPKINTYANFERDDVLPRIKTKIYNAVOIMAIOHSYVASPGYHVR											
			FEAPSRFCTPEDKLSLIDRAHEGLIYMDIYHSSNNNTDGLNMDGDD											

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolus. (Bases 1 to 3360)
 TITLE Nozaki, K., Ito, H., Matsui, H. and Honma, M.
 JOURNAL Phaseolus vulgaris L. mRNA for starch branching enzyme 1
 PUBLISHED ONLY IN Database (1999) In press
 2 (bases 1 to 3360)
 AUTHOR Nozaki, K., Ito, H., Matsui, H. and Honma, M.
 REFERENCE Submitted (03-JUL-1999) to the DDBJ/EMBL/GenBank databases.
 JOURNAL Hirokazu Matsui, Hokkaido University, Faculty of Agriculture, Kita-Ku, Kita 9 Nishi 9, Sapporo, Hokkaido 060-8589, Japan
 (E-mail: mhiro@chem.agr.hokudai.ac.jp, Tel: 81-11-706-2500, Fax: 81-11-706-3635)

FEATURES
 source location/Qualifiers
 1..3360
 /organism="Phaseolus vulgaris"
 /db_xref="taxon:3885"
 /protein_id="BAA82348.1"
 /transit_peptide 133..600
 /gene="kbel1"
 133..2745
 /gene="kbel1"
 /EC_number="2.4.1.18"
 /codon_start=1
 /product="branching enzyme 1"
 /protein_id="BAA82348.1"
 /db_xref="GI:5441246"
 /translation="MYTISGIRFPFVAVLSIHSTLRGDRRAASLPVFLRKNNFSKIL
 AVKSHSDSPSSAIAESKVIIPDHDNSALITOLEPTVITSDANLEDTIEMDE
 DKYNTGEADSSRQLEDIGSVASSPVVDVLPARTSVSVKSVKIPSEVAKPIPR
 PGAGOKIYEIDSLAYRDHDFRGQYKRLHDEINKHGGIDAFSVSDGEGFISRA
 TGITREMAPGAKSALIGDENNNMNPADVMTRNEFGWEIPLPNVDSPPILPISGR
 VKIRMDTSGIKDIPAMIKFESVAPGEPVSGIYDPEPEEKVYFKRPPKPSLR
 IYESHGMSPEPKINTYANPERDVLPRKIKYNAOIMAIQESYVSAKHYNTN
 FAPSRRGTPEDPKSMIDAKHELGLIYLMIDYVHSNNITLDGLMPTGHTFHPG
 SNGYHMDMSRIFNNGSWEVLYLILSNKRWMLDEKTFGEFVDGVTSMYTHGLQVA
 FTGNSEYFGLATVDVAVYLLMLANDLHGLPEPVTIGEIVSGMPTCELPDGGVG
 FDIYLOMAIADMKIILKODEMKMGDIIVTLIRNMLEKCAVAESHDALVSGDKT
 IAFWLMKMDYFMSLDPRATPRIDRGLIKMLITLGMGEGEGLYFMENENGHE
 WIDPFRGDOOLPESVIRGNNYSYDKRGRRFDIGADVLRYRGMEPRRAOHLEK
 GEMTEHOYISKNGEDKVIIFPERKNLVFVFNHNNSYSPYRGCAITPGYKTLVDS
 DDALFEGFNRLNHSAEVITTSBGWIDDRPSFLIYASHTAVVAYALADLEPAFDEVE
 PALADEVEPEEDP"

CDS

polysite 990 a 652 c 735 g 983 t
 BASE COUNT
 ORIGIN
 Query Match 50.4%; Score 1467.4; DB 12; Length 3360;
 Best Local Similarity 80.2%; Pred. No. 0;
 Matches 1723; Conservative 0; Mismatches 426; Indels 0; Gaps 0;

QY 347 ttttgaagtgaagtaataaagaatctgttccaatgcggagacagltagatcaaga 406
 DB 522 ttttgaagtgaagtaataaagaatctgttccaatgcggagacagltagatcaaga 581
 QY 407 aattgatctaaacaaaggtccatccaccgacagaggaagaagaatataagaat 466
 DB 582 ttttgaagtgaagtaataaagaatctgttccaatgcggagacagltagatcaaga 641
 QY 467 agatccaaagcttgacaggtcttcgaacaactagattacacgltatccacagtaacaaag 526
 DB 642 ttttgaagtgaagtaataaagaatctgttccaatgcggagacagltagatcaaga 701
 QY 527 actccgaagaagaattgaagaagtgtgtctgagatgatttctgtgtgtatga 586
 DB 702 atttgaagtgaagaattgaagaagtgtgtctgagatgatttctgtgtgtatga 761
 QY 587 aaagtgtgtcttcgaagcagtaagaagaataactatagagatgagacagagac 646
 DB 762 acgaattgtgtcttcgaagcagtaagaagaataactatagagatgagacagagac 821

QY 647 tacgtgagctgattgattgagatttcaataactggaatccatgcatgcatgac 706
 DB 822 taagtacgagcatttaattgagacttcaacaaattgacaaatgacagatgac 881
 QY 707 tcaagaatgagttgtgtctgagagatcttcttcgcaataatgagatggttaccac 766
 DB 882 tgggaatgagttgtgtctgagagatcttcttcgcaataatgagatggttaccac 941
 QY 767 aattccccatggtcttcgagtaagaatacgaatgatactccatctggcaacaagattc 826
 DB 942 aattccctcatggtcttcgagtaagaatacgaatgatactccatctggcaacaagattc 1001
 QY 827 taltctcgttgatgacagttctcagttcaagcaccagtgtaactccataatgcat 886
 DB 1002 cacttccgttgatgacagttctcagttcaagcaccagtgtaactccataatgcat 1061
 QY 887 atactatgacccctccgaggaagaagatgattgttcaaaaactccagccaagaagac 946
 DB 1062 atactatgacccctccgaggaagaagatgattgttcaaaaactccagccaagaagac 1121
 QY 947 aaactcactcgaattatgagtcgacgcttgagatgagtaacgagccagtaattaa 1006
 DB 1122 aaactcactcgaattatgagtcgacgcttgagatgagtaacgagccagtaattaa 1181
 QY 1007 cactatcccaactttagagatgagtgctccctccatcaaaaagcttgctacatgc 1066
 DB 1182 taccatcccaactttagagatgagtgctccctccatcaaaaagcttgctacatgc 1241
 QY 1067 ttttaagctcgtgctatcgaagacatcatatgctagtttggtatgcac 1126
 DB 1242 ttttaagctcgtgctatcgaagacatcatatgctagtttggtatgcac 1301
 QY 1127 aaactttagcagctagcagcagcagtttggaactccatgatttgaagttcctaata 1186
 DB 1302 aaactttagcagctagcagcagcagtttggaactccatgatttgaagttcctaata 1361
 QY 1187 taaagctcagcagtttagctcttctgttctcattatgatttgcacatgacataac 1246
 DB 1362 taaagctcagcagtttagctcttctgttctcattatgatttgcacatgacataac 1421
 QY 1247 taatcgtttagcagcagcagcagtttggaactccatgatttgaagttcctaata 1306
 DB 1422 taatcgtttagcagcagcagcagtttggaactccatgatttgaagttcctaata 1481
 QY 1307 accacgaggtcatcatgagatgagtgagactcgccttccaactatgagcgtgagat 1366
 DB 1482 accacgaggtcatcatgagatgagtgagactcgccttccaactatgagcgtgagat 1541
 QY 1367 tctaatggtcttcttccaatgcaagtggttggttgatgagatgagatgagatgagat 1426
 DB 1542 tctaatggtcttcttccaatgcaagtggttggttgatgagatgagatgagatgagat 1601
 QY 1427 cagatttgatgagtgagcactcaatgagatgacacccacatgagattgagatttacc 1486
 DB 1602 cagatttgatgagtgagcactcaatgagatgacacccacatgagattgagatttacc 1661
 QY 1487 cgggaactcaaatgagatgagcactcaatgagatgacacccacatgagattgagatt 1546
 DB 1662 cgggaactcaaatgagatgagcactcaatgagatgacacccacatgagattgagatt 1721
 QY 1547 gcttctgaatgagatgagcactcaatgagatgacacccacatgagattgagattgagat 1606
 DB 1722 gcttctgaatgagatgagcactcaatgagatgacacccacatgagattgagattgagat 1781
 QY 1607 taagtgaatgcaacagcttgacatccggttgagatgagatgagatgagatgagatgagat 1666
 DB 1782 taagtgaatgcaacagcttgacatccggttgagatgagatgagatgagatgagatgagat 1841
 QY 1667 tctccacatgagcttgcttgcataaatgagatgagatgagatgagatgagatgagatgagat 1726
 DB 1842 tctccacatgagcttgcttgcataaatgagatgagatgagatgagatgagatgagatgagat 1901

Db 2102 AATTCATATCAGCAAGAAAGCAGATAGAGTAATCGTATTCGAAAGAGGTGATCTCG 2161
 QY 2260 ttcttgatcaatttcattgactagcagcattccgattaccgagttgctcttaa 2319
 Db 2162 TCTTTTCTTTAACTTCACTGACACGACGACTTATTACCGCATGGTGGTCTCA 2221
 QY 2320 agcaggaagaagtaagaatagcttgattgattcagatgattccttgattgagagcttgca 2379
 Db 2222 AGCTGGAATAATATAGATGATTCGATTCGACGACATCTCTTGGTGGATTCATTA 2281
 QY 2380 ggcttagatgatgatgagcagcattgattgagagtgatgacataacggcctgat 2439
 Db 2282 GGTTCATGCAAGGAGGAGTCTTCACTTATGATGGCTTATACAGCAAGCACCCTGCT 2341
 QY 2440 ccttcagtgatcacacacatgataacagcagtgatctatcctttagtgagagatga 2497
 Db 2342 CCTCATGCTGATGACCGCTGATACACCGCTGCTTATGCTTATGCAACACGCA 2399

RESULT 7
 STSBEI 2493 bp mRNA PIN 27-MAY-1998
 LOCUS Solanum tuberosum mRNA for starch branching enzyme II.
 DEFINITION AJ000004
 ACCESSION AJ000004.1 GI:2764395
 VERSION Sbe-II gene; starch branching enzyme II.
 KEYWORDS potato.
 SOURCE
 ORGANISM
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum.
 REFERENCE
 AUTHORS Larsson, C.T.A.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell Research, Genetic Center, Swedish University of Agricultural Sciences, Box 7055, S-750 07 Uppsala, SWEDEN
 REFERENCE
 AUTHORS Larsson, C.T., Khoshnoodi, J., Ek, B., Rask, L., and Larsson, H.
 TITLE Molecular cloning and characterization of starch-branching enzyme II from potato
 JOURNAL Plant Mol. Biol. 37 (3), 505-511 (1998)
 FEATURES
 MEJLINE 98278379
 source
 Location/Qualifiers
 1..2493
 /organism="Solanum tuberosum"
 /plasmid="pALSBE-II (#123)"
 /cultivar="Amanda"
 /db_xref="taxon:4113"
 1..2490
 /gene="Sbe-II"
 /EC_number="2.4.1.18"
 /function="branches 1,4-alpha glucans"
 /product="SBE-II"
 1..2493
 /gene="Sbe-II"
 /EC_number="2.4.1.18"
 /function="branches 1,4-alpha glucans"
 /codon_start=1
 /product="starch branching enzyme II, SBE-II"
 /protein_id="CA03846.1"
 /db_xref="GI:2764395"
 /db_xref="SPRMBL:O49953"
 /translation="EKSSYSESRPSTVAASGVIVPGTOSSSSSSTDOFFETLSP
 ENSPSTVDVSTWEHSAQIKTENDVPEPSDITGSEVLEEDPSSSLDQDGLLESK
 TINTSEITIIDESRIEREGIPPEGLQKITYEDPLTNRHLDYRSQKRLRAI
 DKTBGLFASRGTEKMGFTSRATGITYRMAGCAQSAALIGFNMWDANADIMTRNE
 FGWEILPNNVDSPAIPIHGSRYKIMDPSSGVKSIIPAMINYSLQDEIPYNGIY
 AVPEERYIFQHRPKPKSLRIYESHIGMSPEKINSYVNRDVEIPRIKLIYN
 AVOIMAEIOESHYASFGYHVTNFPAPSSRGFTDDKSLIDKAHEIGIYVLMIVSH
 ASNNTLDGLNMPDGTSCYFHSARGTHMMWDSRLNRYGWEVLRILISNARWLDDEP

BASE COUNT 742 a 445 c 595 g 711 t
 ORIGIN
 KDFGRFDVGTISIMYTHHGLSVGFTGNKYKREPLATDVAVYIYMLVNDLHGLFEDA
 ITTGEVSGMPTFCIIPYODGVSFPDRIRHAIADKRIELKKEDEMRRGDIYHITLN
 RRNSSEKVSVAESHDALVGDKTATWMDKDYDMALDRPSTSLIDGIALHKMR
 LVTWLGEGEYLVNEMNGEHPMIDFPRAEQILDSGSYIPGNSYDRCRRFDLGD
 AEYLRRGLOEFPRAIMOYLEDKKEPMFSEHQFSRDEQGRDMIVFEKMLVVFNFHW
 TKSVDYRIGCLPKGKVALDSDDDPLFGEFGFIDHNAEYFPEGYDPRPSIMVYA
 PSRAVYVALVDKEEEEEEVAVVEVVEE"
 Query Match 47.5%; Score 1384.8; DB 15; Length 2493;
 Best Local Similarity 76.8%; Pred. No. 0;
 Matches 1692; Conservative 0; Mismatches 512; Indels 0; Gaps 0;
 QY 347 tgttgaagaatgaagtaaaagaatctgttccaatcggagagacgttagcacaaga 406
 Db 285 TGGTAAACTGGAGGAGTGCTAAACATTAATTAATCTTGAAGAGACATTAATGATGATC 344
 QY 407 aattgatctaaaccaaggttcattcctccaccggcagaggggaaagaatatatgacat 466
 Db 345 TGATAGGATCAGAGAGAGGGGATCCCTCCAGCTGGACCTTGGTAGAAGATTATGAAAT 404
 QY 467 agatccaagcttgacagcgttcgttccaacacactagattacccgattcacagtacaag 526
 Db 405 AGACCCCTTTTGACAAACTATGCTCAACACCTTGATTACAGGATTCACAGTACAAAGA 464
 QY 527 actcagaagaagaattgacaaagatgaagtgatcgtgagatcttctcgtgataga 566
 Db 465 ACTAGGAGAGCAATGTGACAAAGTATGAGGTGTTTGAAGCTTTTCTCGTGATTAGA 524
 QY 587 aaagttggtttctcagcagcgtgaaacaggaataactataagagatggtggcaccagagc 646
 Db 525 AAAAATGGGTTTCTCTGCTGATGCTTACAGGATCCTACCTGAGAGGGCTCTGCTGTC 584
 QY 647 taagtggcttgatcttgatgagatcttcaataactgaaatccataatgacagatgac 706
 Db 585 CCACTCAGCTGCCTCTCATTTGAGATTTCACAAATTTGGAGCAAAAGCTACATTATGAC 644
 QY 707 tcgaatgagatggtgtgtctcgtggagatcttctgcgaataatgacagatggtccacc 766
 Db 645 TCGGAATGAATTGGTGTGCGGAGATTTTCTCCAAATAATGTGATGCTCTCTGCG 704
 QY 767 aatccccaagcttcgagtaagataagcagatgataactccatctggcaacaagaatc 826
 Db 705 AATTCCCATGCGGCGCAGAGTGAAGATACATATGACACTCCATCGAGTCTTAAGCATTC 764
 QY 827 taitcctgcttgatcaagcttaagttcaagcagcagtgaaatccatataatgacat 886
 Db 765 CATTCCTGCTTGGATCAACTACTCTTACAGCTTCCGATGAGAAATTCATATATGGAAT 824
 QY 887 atctaagatcccccagagagagagagatgattgttccaataatccctcagccaagagacc 946
 Db 825 ATATTATGATCCACCCGAAGAGAGAGATATCTTCCACACCCAGGCGCAAGAAAC 884
 QY 947 aaaaactcagattatagtcagcgttgagaaagagatgagagagagagagagagagag 1006
 Db 885 AAGTGCGCTAGAAATATATGATATCTCATATTTGGAATGAGTAGTCCGAGCCTTAATTTAA 944
 QY 1007 caaatatgccaacttagagatgagatgagcttcctcgcatacaaaaagcttggtacatgc 1066
 Db 945 CTATATAGTAAATTTAGAGATGAAGTTCTCTCCGATTAATAAAAGCTTGGTACAAATGC 1004
 QY 1067 tgttcagatcagctatcattaaagaagatcatatctatgctagtttgggtatcagctcgc 1126
 Db 1005 GGTGCAAAATATATGCTATTTAAGAAGATCTTATTAATGCTAGTTTGGTATCATGCTCAC 1064
 QY 1127 aaactttagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1186
 Db 1065 AAATTTTTCGACCAAGAGCGCTTTTGGAAATCCCGAGACCTTAATCTTTGATTTCA 1124
 QY 1187 taagatcagagatggtgtcttctgtctcagatgatatgttcatagcagatcagcagc 1246


```

gene      VYAPRTAVVYALVDKEEEEEEEVAVVEEVEE"
          2..2512
          /gene="SBE II"
mat_peptide  11..2509
             /gene="SBE II"
             /EC_number="2.4.1.18"
             /product="starch branching enzyme II"
BASE COUNT  749 a      449 c      605 g      720 t
ORIGIN

```

OY	2327	aaatacaagaatagcttggatctcaagatgataccttggatttggagcctttggaagccttag	2386
	2275	AAATATCAAGGTTCCTTGACCTCAGATGATCCACTTTTGGGCGCTTGAGAGAAATGA	2334
Db	2387	tcatgatagcagagacacttgcgtttgaagagtgatgcagataacgcgcctgcagctccat	2446
OY	2387	tcatgatagcagagacacttgcgtttgaagagtgatgcagataacgcgcctgcagctccat	2446
Db	2335	TCATATATGCCGAATTTTCACCTTTGAAGATGATGATGATCGCTCGTTCATATAT	2394
OY	2447	ggtttacacacacatgtagaacaacatgctgctcgtttagtggagagatggaagtggagaa	2506
Db	2335	GGGTATATGCACCTTGTAGAATCAGCAGTGTCTATGCACATAGTAGAACAAGAAGAAAGA	2454
OY	2507	tgaattggaa	2516
Db	2455	AGAAAGAAAGAA	2464

RESULT	9				
A58169				PAT	05-MAR-1998
LOCUS	A58169	2578 bp	DNA		
DEFINITION	Sequence 19 from Patent WO9634968.				
ACCESSION	A58169				
VERSION	A58169.1	GI:3713894			
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1	(bases 1 to 2578)			
AUTHORS	Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R., Sidebottom, Christopher,M. and Westcott,R.J.				
TITLE	IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION Patent: WO 9634968-A 19 07-NOV-1996;				
JOURNAL	NAT STARCH CHEM INVEST (US) Other publication AU 5509996 961121.				
COMMENT					
FEATURES	Location/Qualifiers				
Source	1..2578				
	/organism="unidentified"				
	/db_xref="taxon:32644"				
BASE COUNT	770 a	462 c	616 g	730 t	
ORIGIN					

Query Match	Similarity	Score	DB	Length
Best Local Similarity	77.3%	1381.2	9	2578
Matches 1677:	Conservative %	0	Mismatches 493:	Indels 0:
			Gaps	
Qy	347	tttttaagaataaagaataaagaatcgttcccaatgsgggagacattgacatcaga	406	
Db	350	tggtaaacgcgagagctttaaacttaaaacttaacittcggaagacacattatgatgatac	409	
Qy	407	aattgattcaaccaagatcatcttcctccacccggcagaggggaagaataatgacat	466	
Db	410	tgatgatcatcagagagagggccatccctccacccggacattgctcagaagaattatgaan	469	
Qy	467	agatccaagcttgacaggcttcgtcaacacactgattaccggtattccacgatacaag	526	
Db	470	agaccccccttttgacaacactatcgtcaacaccttgatttacaggatttacaagtaacaga	529	
Qy	527	actccgagaagaacttgacaagatgaagagtgcttgatgcatcttcctcgtgcatga	586	
Db	530	actgacggcagccaaattgacaagatgagagggtttggacaccttttctcgtgattatga	589	
Qy	587	aaagtgtggtttctcagcagatgaagaacagagataactatagaagtgaggacacagagc	646	
Db	590	aaaaatgggtttcacttcgtaagtcacagcagatatacctaaccgtgaggggctctcgatgc	649	
Qy	647	taacgtggctgcattgatttgagaatttaataaacatcgaatactctatgcacatgacac	706	
Db	650	ccagtcagctgccttcatttgagattttacacatttgagaccacaattgctgacattatgac	709	
Qy	707	tcagaatgagtgatgtcgtcgtggagatccttttgcgaataaagcagatggtttcaacc	766	

Db	710	TCGAAATGAAATTTGGTGTCTGGGGAGATTTTTTCTGGCAATTAATGTGATGATGCCTCG	769
Oy	767	aattccccaatggtctccgaatgaatgacgaatgatactccatctcctcggcaaaaagatcc	826
Db	770	AATTCCTCAATGGGTCCAGAGCTGAAGATAGTATGAGACACTCCATCAGGTGTAAAGATTC	829
Oy	827	tattccttgcttggatccaagttctcagttcaagcaccaagtgtaactccatataatggcgt	886
Db	830	CATTTCGGCTGGATCAACTACTCTTCACAGCTTCTCTGATATAATTCCATATATAGGAT	889
Oy	887	atactatgatctctccgaagagagagaagtatglttccaaaaatcccaagccaaagagacc	946
Db	890	ATATTATGATCCACCAGAAAGAGAGGATATATCTTCACACACCACGGCCAAAGAACCC	949
Oy	947	aaaaacacttcgattatlatagtcgaacttggaatlagtaagtaaggagccagtaattaa	1006
Db	950	AAATCTCGCTGGAAATATATGAAATCTCATATTTGGAAATGATGTCCGGAGCCCTAAATTA	1009
Oy	1007	cacatagccaactttagagatgatgltgcttctccgcactcaaaaagcttggctacaatgc	1066
Db	1010	CTCATACGTGAATTTTGGAGATGAAATGATCTTCTCTCGCATATAAAAAAGCTGGGTCAATGC	1069
Oy	1067	tgttcagctatggtcctatcaagaagatccatattatcctcagtttggatctacgcgtcac	1126
Db	1070	GGTGCAAAATTTATGGCTTTTCAAGAGCAATCTTATATGCTAGTTTGGTATTCATGTCAC	1129
Oy	1127	aaactttatbcacatcagcagccgcaatttggaactcctgaattttaaagttctcaataga	1186
Db	1130	AAATTTTTCACACAGACGACGGTTTGGAAAGCCCGCCAGCTTAAGTCTTGTGAATGA	1189
Oy	1187	taaaagctcagagttgaagtctctcttctcctatgatatgtgtctcaatagcactatcaac	1246
Db	1190	TAAACCTCATGAGCTAGGAATGTGTTGTTCCATGAGCAATGTTTCACACCATGATCAAA	1249
Oy	1247	taatcagttgaatgagctgataatgatttitaatgtaagatgtaagatgtactactctcgtg	1306
Db	1250	TAAATCTTAAATGAGACTGAAACATGTTTAAAGCCACCCAGTAATGTATCTTGTCACTGTGG	1309
Oy	1307	accacggggatcaatattgagttatgggaactctgcgctttcaactatgaggaagctgagaggt	1366
Db	1310	AACCTGATGATTAATGATGAGATGAGATTCGCCCTTTTAACTATGAAACCTGSGAGGT	1369
Oy	1367	tctaaagttctctcttccaatgcgaagtggttggtgataagatgatacaagtttgggtt	1426
Db	1370	ACTTATGATATCTCTCTCAAAATGGAGAAATGAGTGGTGGATGAGTTCAATTTGATGGATT	1429
Oy	1427	cagatttgcggggtgactccaatgatgatcaacccatctagaatgcaggtgagtatttacc	1486
Db	1430	TGAGATTGATGGTGTGACATCAATGATGATGATCTCAACACGGATTTATGGGTGACATTCCAC	1489
Oy	1487	cggcaactacaatgatgaacttcttggaatctgcgaactgtatgagatgcttgggttttltgat	1546
Db	1490	TGGGAACATACGAGGAATACCTTTGAGCTACGCACTGATGATGGAGTGGCTGTGTATTCAT	1549
Oy	1547	gctgttgaatgatatgatatcaatggtctctctccagaagctgtcaacaaatggttgatagagt	1606
Db	1550	GGTGGTCAACGATCTTATATCTATGCGCTTTTCCAGATGCAATATACATATGGAGAGATGT	1609
Oy	1607	taattggaatgcacaagaatttgatctccggtttgaaagtgggtgggttgatctgtattacg	1666
Db	1610	TAGCGGAATGCGCAATTTTGTATTTCCGTTCAAGATGGGGGTGGTGGCTTTCATTCG	1669
Oy	1667	tctcccaatgagctgtctgtctgataaagtgtttgagattatctcagaagaagatgatgaattg	1726
Db	1670	GCTGCATATGGCAATGCTGATTAATGATGATGATGCTGACAGAAACGGGATGAGGATTCG	1729
Oy	1727	gaaatagggtgacatgtacatatgctgcacaacaagaagcgggttggttgaaaagtgtgttc	1786
Db	1730	GAGAGTGGGTGATATGTGTATATACACTGACCAATATGAAGATGGCTCGAANAAGTGTGTTTC	1789
Oy	1787	ttaagttaaaatctatgacagagccctgtttgtgtgaaacaaactgtaccttttjgctgat	1846
Db	1790	ATACGTGAAATCATGATCAAGCTTAGTGTGCGGTGATAAACATATGCAATCTCTACGTAT	1849

OY	887	atactatgatctcccgaggaggaagtatggttccaanaatccctcagccgaagagac	946
Db	1196	ATATTATGATCCACCACCAAGAGAGAGATATGCTTTCACAAACCACGGCCAAAGAAAC	1255
OY	947	aaaatcacttcggatttatagtacgcacgttggaaatgagtagcagagccgaattaa	1006
Db	1256	AAAGCGCGTAGATATATATGATCTCATATTGGAAATGAGTCCGAGCCTAAAAATTAA	1315
OY	1007	caactatgccaactttagagatgatgtgcctctctgcatacaaaaagcttgctacaatgc	1066
Db	1316	CTCATACGTGATTTTAAAGATGAAGCTTCTCTCCATCAAAAAAACCTTGGGTACAAATGC	1375
OY	1067	tgctcagctcatggtcattcaagaacatcatactatgcatttggatctggatccagtcac	1126
Db	1376	GGTGCAAAATATGGCTATTTCAGAGCATCTTATTATGCTAGTTTGGTATCATAGTCCAC	1433
OY	1127	aaactttagcagctcagccagccgatttggacctctgatgatlttaagtctcataga	1186
Db	1436	AAATTTTATTTTGGCACCAAGACGGCTTTTGGACGCCCGACGACCTTAACTTTGATTGA	1495
OY	1187	taaaagctcagcagcttagtctctctgtcttcacagatatgttttcaatagcagatcac	1246
Db	1486	TAAAGCTCATGAGCTAGGAATGTGTCTTCATGAGCAATTGTTCACAGCAGCATGCATCAA	1555
OY	1247	taatacgttgaatggccttgaataatgtttgatacgaatggtcacaacttcaactctgcg	1306
Db	1556	TAAATACCTTATAGATGAGTCAACATGTTTGGACGGCAGATAGTGTATTCTTCACTCTGG	1615
OY	1307	acacaggggtacatcatgttagtctgtgggaactctgccttcaactcttggagagcttggagt	1366
Db	1616	AGCTCGTGGTATATCATATGAGATGTGGGATTTCCGCCCTTTAACTATGAGAACTGGGAAGT	1675
OY	1367	tctaaagtcttctcttccaatctgaagatggtgtgttggatacgaatctgaatggtgt	1426
Db	1676	ACTTAGGATCTTCTCTCAATATCGAGATGGTGTGGATGAGTGCAAAATTTGRTGAT	1735
OY	1427	caagtttagaggggtgacttcaatgatgttaacacctatlgatgtcaggtatgaatttac	1486
Db	1736	TAGATTGTAGTGTGTGACATCAATGATGATATCTCCACCGAGATTATCGTGGATTTAC	1795
OY	1487	cggacaactcaatgaacttcttgatatacgaacttgatagatgctgttgattatgat	1546
Db	1796	TGGGAAGTACGAGGAATACCTTTGGACTCCGCACTGATGTRGATGCTGCCGTATATCTAT	1855
OY	1547	gcgtctgaatgatatagatatacgtctctctccagaagcgtcaccaatggtgaagaatgt	1606
Db	1856	GCTGGCCAAAGATCTTATTCATGGGCTTTCCACAGATGCATTTACCATGTGGTGAAGATGT	1915
OY	1607	tagtggagaatccaaacagtttgcattccgttgaagatggtgtgtgtgttattatcag	1666
Db	1916	TAGCGGATGCGACATTTTGTATTCGCCGTCAAGATGGGGGTGTGGCTTTGACTATCG	1975
OY	1667	tctccacatggtctgttctatataaactgggttgaagatatactcagaagagagataagatcg	1726
Db	1976	GCTCATATATGGCAATTTCTGTAATAATGGAATGTAGTTGCTCAAGAAACGGAGATGG	2035
OY	1727	gaaaatgtgtgacattgttatacatatgctgcacaaacagcggtgtgttggaaaatgtgttctc	1786
Db	2036	GAGAGTGGGATATTTGTTTATCATCACTGCACAAATATATMAATGCTGGGAAAGTGTGTTTC	2095
OY	1787	ttaatgcgaagtcatbaacagcccttgtgttgacaacaaatcttgatttggctat	1846
Db	2096	ATAGCTGGAAGTCAATCATCAACCTTACTCGTGTATTAACCTATATAGCATTTCTGGCTAT	2155
OY	1847	ggacaaagatatgatacctaactcagctctgcacagacacatctactctctcaatagtcg	1906
Db	2156	GGACAAACGATATGATGATTTTATGTGCTTTGGATAGACCGGTCAACATCATTAATATGATCG	2215
OY	1907	tgaggtagcattcaaaaatgtagcgtttttaccatggatataagcagagaaagata	1966
Db	2216	TGGATATGCAATGCAAGATGATATAGGCTTTGAACTATAGGATTAAGAGAGAAAGGGTA	2275

Query Match	Best Local Similarity	Score	DB	Length
Matches 1677; Conservative	77.3%	491	Indels 2; Gaps 1	

QY 347 tcttgaagatgaagtaataaagaatctgttccaatgcggagacagttagatcaga 406
 Db 350 TGGTAAACTGAGAGAGCTCTAAACATTTAAATACCTTCTGAAGACATTAATGATGAATC 409
 QY 407 aattgatacacaagaagccatccctccaccggcaagggcaagaatataatgacat 466
 Db 410 TGATAGGATCAGAGAGAGGGGACCTCCACTGAGACTGTGCACAAATATTATGAAT 469
 QY 467 aggtccaaagcttgcagagcttgcacaacagatccagttaccgattatccagtaacaag 526
 Db 470 AGACCCCTTTTGCACAAACATATGCTCAACACCTTGATTAACAGATATTCACAGACAA 529
 QY 527 acctcagaagaataatgacagaatataaagtagtctgagatcttcccgtagtata 586
 Db 530 ACTGAGGAGGCAATGATACAGATAGAGGTGGTTGGAGCTTTTCTCGTGTTATGA 589
 QY 587 aaagtttgcttccacgacagtgaaacaggaataactatagaagtgagcaccagagc 646
 Db 590 AAAAATGGGTTTACTGCTAGTCTACAGGTATACCTTACCGTGAAGTGGCTCTGCTGC 649
 QY 647 taagtggctgcatttgtagaatttcaataactggaatcctaagtcagatgltcagac 706
 Db 650 CCAATGAGCTGCCCTCATTTGAGATTTCACAAATTTGGACGCAAAATGCTGACATTTATGAC 709
 QY 707 tcaagaatgagtgtagtctcgagagatcttcccgaaataagtcagatgagttaccacac 766
 Db 710 TCGGAATGAATTTGTGTCTGGGAGATTTTCTGCCAAATATGTGATGTGCTCTCTGC 769
 QY 767 aattcccatggttctcagtaagaatagacatgagatctccatctggaacaagaatctc 826
 Db 770 AATTCTCATGGGTCCAGAGTGAAGATACGTATGAGACATCCATCAGGTCTTAAGATTC 829
 QY 827 tattcgtgcttgatcaagttcctcaagtcagaacagtgaaatcccatataatgcat 886
 Db 830 CATTCTGCTTGGATCACTACTC--TACAGCTTCTGATGAATTCATATATATGAAT 887
 QY 887 atactaagatccctccgagaggaagtagtglttcaaaaatccctccagcaagaagac 946
 Db 888 ATATATGATCCACCCGMAAGGAGAGGTATATCTTCCAAACCCACGCGCAAGAAAC 947
 QY 947 aaatccatccgagattatagtcagcagttggaatgagtaglacagagccagtaata 1006
 Db 948 AAATCTGCTGAGATATATATATCTCATATTGGAATGAGTAGTCGAGGCTTAAATTA 1007
 QY 1007 cacaatgcaaacctttagagatgagtggtctcccgatcaaaaacgttgctacaatgc 1066
 Db 1008 CTCATAGCTGAATTTAGAGATGAAAGTCTTCCGCGATAAAGGCTTGGTGAACAATGC 1067
 QY 1067 tgttcaagctatagctatccaagaacatcatatagtcagtttgagatcaagtcac 1126
 Db 1068 GCTCAATATATGCTATTCAGAGCATCTTATATAGTATGCTTGTGTTATCATGTCAC 1127
 QY 1127 aaactttatgagcgtcgagagccagattggaaccccgatgatttaagctctataa 1186
 Db 1128 AAATTTTGTGACCAAGCAGCCGTTTGGAAACCCCGAGACCTTAAGCTTTGATGA 1187
 QY 1187 taaagctcagagttaggtctctgtctcagatgatalatgttcaatagcagatcacaac 1246
 Db 1188 TAAAGGCTATGAGCTAGGAATGTTGTTCTCATGAGACATTTGTTACAGCCATCATCA 1247
 QY 1247 taaatagctttagatgagcagatagtttga tggtaacagatgcaactacttcaactc 1306
 Db 1248 TAAATCTTATGATGATGATGAACATGTTTGAAGGACCGATAGTGTGTTACTTTCAC 1307
 QY 1307 accacgggagatcatgagatgagtgagacatcgcccttcaactatagggagcggagag 1366
 Db 1308 AGCTCGTGTTATCATTTGATGGAGTCCCGCTTTTAACTATGAAACTGGAGGT 1367
 QY 1367 tctaaagttcttcttcaaatgcaagtgagttgagatgagtaaaagttatgagtt 1426
 Db 1368 ACTTAGATCTCTCTCAAAATGCGAGATGCTGTTGATGAGTTCAAATTTATGATG 1427

QY 1427 cagattgagtgagtgatcttaatatgatacaccatcaatgagttcaggtatgttacc 1486
 Db 1428 TAGATTTATGCTGTGATATCAATGATGATATATACACCGAGATTAATCGGATTCAC 1487
 QY 1487 cggcactacataatlaacttcttgatataagcaactgataatgagtgagttatgtat 1546
 Db 1488 TGGGCAATGACAGGAATGCTTTGACATCGCAACGATGTGATCTTGTGTATGAT 1547
 QY 1547 gctgtgatatataatgataatgagtgagtgagtgagtgagtgagtgagtgagtgag 1606
 Db 1548 GCTGTCAACCATCTTATTCATGAGGCTTTTCCAGATGCAATTTCCATTTGATGAT 1607
 QY 1607 tagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1666
 Db 1608 TAGCGGAATGCGGACATTTTGTATTCGGTTCAAGATGGGGGTGTGGCTTGCATTCG 1667
 QY 1667 tctcagatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1726
 Db 1668 GCTGCAATGAGCAATGCTGTATTAATGATGATGATGATGATGATGATGATGAT 1727
 QY 1727 gaaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1786
 Db 1728 GAGAGTGGGTGATATTTGTTATACACTGACAAATGAGAGATGTCGCAAAAGTGTTC 1787
 QY 1787 tcatgctaaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1846
 Db 1788 ATACGCTGAAGTCAATGATCAAGCTCTGATGATGATGATGATGATGATGATGAT 1847
 QY 1847 ggaagaagatagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1906
 Db 1848 GGACAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1907
 QY 1907 tggatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1966
 Db 1908 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1967
 QY 1967 ttgaaattttaggaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2026
 Db 1968 CCTAATTTTCAATGAGGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2027
 QY 2027 tctacatctcccaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2086
 Db 2028 ACACACCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2087
 QY 2087 gcttagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2146
 Db 2088 ACGGAGATTTGACCTGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2147
 QY 2147 tcaagaatctcagatcttgaagaagcctatggttctcagtgagtgagtgagtgagtgag 2206
 Db 2148 CCGGCTATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2207
 QY 2207 atcagaagaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2266
 Db 2208 ATCAGGAAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2267
 QY 2267 atcagaatctcagatcttgaagaagcctatggttctcagtgagtgagtgagtgagtgag 2326
 Db 2268 CTTTATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2327
 QY 2327 aaatgagaatagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2386
 Db 2328 AAATATCAAGCTTGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2387
 QY 2387 tcatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2446
 Db 2388 TCATATGAGCGGATATTTACCTTTGAAGGATGATGATGATGATGATGATGATGATGAT 2447
 QY 2447 ggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 2506
 Db 2448 GGTGATGAGCTTTAGAACGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 2507
 QY 2507 tgaattgaga 2516

```

Db      2508 AGAAGAGAA 2517
RESULT  13
LOCUS   STU011888
DEFINITION Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE A-4.
ACCESSION AJ011888
VERSION   AJ011888.1 GI:4584508
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE    Potato.
ORGANISM  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS  Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M., Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
TITLE     A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure, cloning and characterisation of multiple forms of SBE II
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 2982)
AUTHORS    Jobling,S.A.
TITLE      Direct Submission
JOURNAL    Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK

FEATURES
Source
1..2982
/organism="Solanum tuberosum"
/cultivar="Desiree"
/db_xref="taxon:4113"
/note="sequence SBE A-4"

transit_peptide 140..283
/gene="SBE II"
140..2776
/gene="SBE II"
/standard_name="1,4-alpha-glucan branching enzyme"
/EC_number="2.4.1.18"
/codon_start=1
/product="starch branching enzyme II"
protein_18="CAB40746.1"
/db_xref="GI:4584509"
/translation="MYYTLGSGVRPPYVSVKSNQFSSNGDRNRANISVLEKKHSLSR
KILAEKSSVNSERSPTIAAGKVLVPGIQSDSSSSSTDOFEAEFSPESPSTMDV
SSTMEHSAQIKTENDVPSDLGVSPEIDPSASLOLOCGGLSEKTLNISEETII
DESDRIRRGIPPGIGOKITEIDPLITNRQHLDTISQKRLREALIDYEGLEAF
SRGYRMRGFTSRATGITYREMAFGAQSALIGFNMMDANADMTNRENGVEIFLPI
NVDSFPAIPHGSRYKIRMDPPSGVKSDIPAMINYSLQDPDEIPYNGIYDPEERYI
FOHPRPKKSVRIYESHIGNSPEPKINSYVRDEVLPRIKLGINVAVOIAQDH
SYVAFGHTVNFAPSSRFQTPDLKSLDKAHLEIGIVLMIVHSHSNNTLDGHN
MFDGDSQYFHSRGARYHMMWDFLENYGMVRLRYLISARWMLDEFPDGRPGV
TSMCTHGLGVSFTGNVEYFRLATVDVAVVYLMVNDLISLEPDAITTGEDVSGM
PTPCVPYODGSGVCDYRLHMAIDAKTEILKKDEDEMRGDIHTLTNRWSEKCVSY
AESDQALVGCKTIAFWLMDKMDYDEALDRPSTSLDRKIALHKMRITVATGLGEG
YLNWNGEFGKPIAWIDPRAEOHLSDSVIPRNOFSDCKRRFEDGDAEYLRRLQ
EFDRAMQYLEDKYEFTMSHQFLSRKDEGRMTVPEKGNLVEFNFHMTKGYSDRIG
CLKPGKYKVALDSDPLPFGGFGRIDHNAEYFTFEGWYDPRPSIMVYASRAVYAL
VDRKEEEEEVAAVEEVVEE"
140..2776
/gene="SBE II"
284..2773
/gene="SBE II"
/EC_number="2.4.1.18"
/product="starch branching enzyme II"

BASE COUNT 888 a 529 c 703 g 862 t

Query Match 47.0%; Score 1370.4; DB 15; Length 2982;
Best Local Similarity 76.4%; Pred. No. 0;

```

```

Matches 1683; Conservative 0; Mismatches 521; Indels 0; Gaps 0;
QY 347 tttgaagatgaagaatgaatgaatctgttccaatgcygagagattagatcaaga 406
D 568 TGTAAACTGGAGAGAGCTTAAACATTAACTTTGAAAGACACATATTGATGAAATC 627
QY 407 aattgatactaaaccaaggtccatccaccggaagaggaagaatalatgacat 466
D 628 TGATAGGATCAGAGAGAGGGGATCCCTCACCCTGACTTGGTCAGAAATTTATGAAT 687
QY 467 agatccaagcttgacagagcttcgtcaacaactagattccggtattcaagtaacaag 526
D 688 AGACCCCTTTTACAAACTATGTCACACCTTGATTCAGGTATTCACACTACAAAGAA 747
QY 527 actccgaagaatattgacaagatgaagtagctcgtgagtagtattctcgtggtatga 586
D 748 ACTGAGGAGGACCAATTGACAAAGTAGAGGTGGTTTGGAAAGCTTTTCTCGGTTATGA 807
QY 587 aaagttggttctcaccgcaagtgaacaggaaataactatagagagtgagcaccagagc 646
D 808 AAGAAATGGGTTTACATCGATGCTACAGGTATCACTTACCGTGAAGTGGCTCTGTGTC 867
QY 647 taagtggctgcattgattggagatttcaataactggaatccatagatgcatgac 706
D 868 CCAATCAGCTGCCCTCATTTGGGATTTTCAACAATTTGGACGGAATVGTCACTTATGAC 927
QY 707 tcagatgagtgatgctgctgagagatcttttgcgaataatgagatggttcaaccac 766
D 928 TCGGAATGAAATTTGGTGTGGAGATTTTCTGCAATAATATGATGATGTTCTCCGTC 987
QY 767 aattcccaatglttcacggttaagataacgcatgagatctcatctgcaacaagaatlc 826
D 988 AATTCTCATAGGTCACGAGTGAAGATACGATGACATCCTCATCAGGTGTTAGAGATTTC 1047
QY 827 tattctgttgatcaaatctcagttcaagaacagagtgactccatataatgcat 886
D 1048 CATTCTGCTTGATCACTACTCTTTTACAGTTCTCTATGAAATTCATATTAATGAAAT 1107
QY 887 atactatgctctcccgagaggaagatgattgttcaaaaatcccaagcaagaagac 946
D 1108 ATATTATGATCCACCGAAGAGAGAGATATATCTTCCACACCCACGCGCAAGAAAGAC 1167
QY 947 aaatcactcggatgaagtagcagcttggaatgagtagtgaggaagcgaagataa 1006
D 1168 AAGTGGGAGAAATATATATGATATCATATTTGAAATGATGATGTCGGAGCCTTAATAATTA 1227
QY 1007 caacatgcaacttagagatgagatgctctcctcgcacatcaaaaagcttgctacaatgc 1066
D 1228 CTCATACGATGATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1287
QY 1067 tcttaagctcaggtatctccttcttctcaatgagatgattgagtagtattgggtatacagtcac 1126
D 1288 GGTGCAATTAATGCTATTCATTCAGACATCTTATGCTATGCTATGCTATGCTATGCTATGCTATG 1347
QY 1127 aaactttagcagcttagcagccgatttggaaccccgatgattaaagcttataaga 1186
D 1348 AATATTTTGGACCAACAGACAGCGTTTGGAGACCCGAGACACTTAAAGCTTTGATGTA 1407
QY 1187 taaagctcaagatgagttccttcttctcaatgagatgattgagtagcattgacatcaac 1246
D 1408 TAAAGCTCATGAGCTAGGAAATTTGTTCTCATGATGATGATGATGATGATGATGATGATGATG 1467
QY 1247 taatacgttgatgagcgaatgattgattgaggaagatgagcacttcaactctcg 1306
D 1468 TAATCTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1527
QY 1307 accaagggatcatattgagatgagcctcgccttccaactatgagagagagaggt 1366
D 1528 AGCTGCTGTTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1587
QY 1367 tctaaagttcttcttcaaatgagagtgagtgattgagtagtacaagttgattgaggt 1426
D 1588 ACTTAAATCTCTCTCAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1647

```


OY	1127	aaactttatibgcagctgacgacgcgaatttggaactctctgatagtttaagtcctctaata	1186
Db	1348	AAATTTTTTGCACCAAGCACCCGTTTTGGAAAGCCCGGAGACGACCTTAAATCTTTTATTGA	1407
OY	1187	taaagctcaacgaagttaagctctctgtcttcacatgataatgttcaatagacgaataac	1246
Db	1408	TAAACCTCATGAGCTAGGAATGTGTGTCATGAGCAATTTGCCACAGCATGCATCAA	1467
OY	1247	taatacgtttggaatggcctggaatatagtttgatacagatgylcaacttaactctactc	1306
Db	1468	TAAATCTTTAAATGAGACCAACAACTTTTGACTCCACCGATAGTGTAACTTCACTCTCG	1527
OY	1307	accacggggatcaatctggatgagtggagctctgcctttcaactcttggaagcttggaag	1366
Db	1528	AGCTGTGGTTATCATTTGGATGGATGTCGCCCTCTTAACTATGAAACTGGGAAGT	1587
OY	1367	tctaaagttctctcttccaatgcgaagtggttggttgatagtaacaaagtltgatlyglt	1426
Db	1588	ACTTAAAGATATCTTCCCAATATGGAGATGCTGTGGATGCGTTCAATTTGAATGAGAT	1647
OY	1427	cagatttgaagggtgactccaatagatgataccctcaatgattgcaggtagatattac	1486
Db	1648	TAGATTTCATGCTGTGCATCAATGATGATATTCACACGATTAATCGGTGGATTAC	1707
OY	1487	cggcaactacaatgaataactttggaatagcaactgatagtatgctgtgttaattgat	1546
Db	1708	TGGGAAGTACAGAGAAATACTTTGGACTCGCAACTGATATGATGCTGTGTATCTGAT	1767
OY	1547	gctgttgaatgatactgatttcaatgactctctccagaagctgcaccatttgtaagaat	1606
Db	1768	GCTGGTCAACGATCTTATTTATGAGGGCTTTTCCAGATGCAATTAACATTTGTGAAGATG	1827
OY	1607	tatggaatgtccaacagattgcaatccoggttgaagaatggttggttgcttgattctg	1666
Db	1828	TAGGGGAATGCGGCACATTTTGTATTCGCCGTCCAAAGGGGGGTGTGGCTTTGACTATCG	1887
OY	1667	tctccaatggtcgtgtgcgataaatlyglttagattatlcgaagagagaatgaattg	1726
Db	1888	GCTGCATATGTCATTTCTGATTAAGAGGAAATGGATGGATGGTCTCAAGAAACGGATGAGATWG	1947
OY	1727	gaaatgtgtgaacttgttaatatgtcttgacacaaagcggtgtgttgaaagtgtgttc	1786
Db	1948	GAGAGTGGGTGATRTTGTATTATCACTGTCAAAATPAAMATGCTGGAAAGTGTGTTTC	2007
OY	1787	ttaatgtgaagtatgacacgaagcccttgttggtagcaaaactatgatttgctgcgat	1846
Db	2008	ATACGCTGAAGAAGTCATGATCAACGCTTAAGTCGGTATAAACTATATAGCATTTCTGGCAT	2067
OY	1847	ggacaagatagtatgacttaactgtgcttttgacagacatactactctctcataatgc	1906
Db	2068	GGACAAAGATATGATGATTTATTTAGCTCTGTGATGACCCGTCAACATCTAATTAATAGATCG	2127
OY	1907	tggagtagcaatgcacaaatgtatcagctcttaacatggatattagcgagaagata	1966
Db	2128	TGGGATGTGCTGCACAAATGATGATGCTGTAACTATGGGATTTAGAGAGAGAAAGGTA	2187
OY	1967	tttgaatttatagggaatgaaatttggacaccccgagtggatgatttccaaagtgta	2026
Db	2188	CTTAAATTTTATGGGAAATGAATTTGGCCACCCCTAGAGGATTAATTTCCCTAGCGCTGA	2247
OY	2027	tctacatcttcccagtggttaatttgttctctgggaacaattaaagttaataatgcg	2086
Db	2248	ACAACACCTCTCGATGGCTCACTAATCCCGGAAACCAATTCAGTTATGATTAATGACG	2307
OY	2087	gcgttagtttgatctaggaacttcaaaagcatctgataataatgaaatgcaagatttca	2146
Db	2308	ACGAGATTTTGACCTGGGAGATGCAAGAAATTTAAGATACCGTGGGTTGCAGAAATTTGA	2367
OY	2147	tcaagcaattcagacatttgaagaagccatagtttcttgactctgagacaaccaatcat	2206
Db	2368	CCGGCCATACGATCTTGAAAGATTAATATGATTTATATGACTTCAGAAACAGTTTCAT	2427

QY	2207	a t c c g g a a g a t b a a a g g a t c g g a t c a t t g c t t c c g a a g g g a a a c c t g u t t t g t	2266
Db	2428	A T C A C G A A A G S G T S A A C G A C A T A G C A T G A T G T A T T T G A A A A A G G A A C C T A G T T T T G T	2487
QY	2267	a t t c a a t t t c a t t g a c t a g c a g c a t t c o g a t t a c o g a g t t g g c t g t t a a g c c a g	2326
Db	2488	C T T T A A T T T T C A C T G G A C A A A A A G C T A T T C A G A C T A T C C A A A G C C T G C T G A A A C C T G G	2547
QY	2327	a a g t a c a a g a t a g t c t g t a t t c a g a t a t c c t t g t t t g a a g c t t g c a a g c t t a g	2386
Db	2548	A A A T A C A A G G T T G C C T T G S A C T C A A T A T G A T C A C T T T T T G G T G G C T T C G G A G A A T T G A	2607
QY	2387	t c a t a g a t g c a g a g c a c t t c a g c t t t a a a g g t g t g a c g a t a a c o g g c t c o g a t c c t c a t	2446
Db	2608	T C A T A A A G C C G A A A T T T C A C C T T T A A A G A A G T A T G A T G A T C C T C C T G T C A A T A T A T	2667
QY	2447	g g t g t a c a c a c t l g t a a a c a c a g t g t c a t c t c t t a g t g g a g g a t t a a g t b g a a a	2506
Db	2668	G G T G T A T G C A C C T T G T A A A A C A C A C A G T G G T A T G A C T A G T A G A C A A A A A A A A A A A A	2727
QY	2507	t g a a t t g g a a c c t g t c o g c g g t a a g a t a t a t c c t a a c a c a c a g t t c t g a a g c a a g a t y	2566
Db	2728	A G A A G A A G A A A A A A A A A A C T A C C A C A C A G T A G A A A G A A G T A G T A G A A G A A G A A T G	2787

Search completed: August 10, 2001, 12:48:50
Job time: 8137 sec

Fri Aug 10 16:32:37 2001

us-09-297-703a-28.Aug9.rge

Page 24

Db 1671 TCCTGTGATATGATGATTCACGCTCTTCCCTGAGGCTGTTACCATGTTGTAAGATG 1730
 Qy 1606 ttagaggaatgcgaacagcttgcctccggttggaagatggggtgtgtcttgattatc 1665
 Db 1731 TTACGGGAAGGCAACATTTTGCATTCAGTGAAGATGGTGTGATTTGATTAAC 1790
 Qy 1666 gtcccaatagctgtctgtgaataatgggttgattatccaagaagatgaagatt 1725
 Db 1791 GTCTCCACATGGCCATTCGCCGTAATAGATTCATTTAAGAAAGACATGAGGACT 1850
 Qy 1726 ggaataatgggtgaacatgtgaacatgtgacacacagcggtgtgtggaagatgtgtt 1785
 Db 1851 GGAATAATGGGTGACATTTGCTACACACACACAGAAAGGTTGGTGAATAAAGTGTG 1910
 Qy 1786 ctatagctgaagatgaacacagcggtgtgtgtggaacacacatttgattgtgtcga 1845
 Db 1911 CTTATGCTGAAGATGATGACCAAGCTCTTGTGTGTGAACAAATATTCATTTGGCTGA 1970
 Qy 1846 tggacaaggaatgtatgactatgctctgtgacagacacactactctctctatagac 1905
 Db 1971 TGGACAAGGACATGATGACATTCATGCTCGTGAAGACATCTACTCTTATATGATC 2030
 Qy 1906 gtggagtagcattgcacaaatgatcaggtcttattacacatgggattagcggaagat 1965
 Db 2031 GTGGAATGACATGACAAATGATGACAGCTTATACCATGGCTTACGCGAGAGGAT 2090
 Qy 1966 attgaatttatgggaatgaattggacacacacacagctgattgatttcccaagagtg 2025
 Db 2091 ATTGAATTTATGGGAATGATGATTTGACATCTGATGATGATGATTTCCAAAGAGGG 2150
 Qy 2026 attacatctccacagtggaattgttctgtggaacacacatgataatgattc 2085
 Db 2151 ATCGACATCTGCCCATGATGATTAAGTAATTCAGGGAACACCAAGTATATTAATGCC 2210
 Qy 2086 ggcgaagttgattgattgaacacacacacacacacacacacacacacacacacacac 2145
 Db 2211 GTCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2270
 Qy 2146 atcaagac 2205
 Db 2271 ATCAGGCAATGACATCTTGAAGAGGCTATGATGATGATGATGATGATGATGATGATG 2330
 Qy 2206 tcaacggaagatgaagagatcgatcattgtcttcgaaggggaacacacacacacacac 2265
 Db 2331 TATCAGGGAAGATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2390
 Qy 2266 tattaatttcatgtagcagcattgtgattacacacacacacacacacacacacacacac 2325
 Db 2391 TATTCATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2450
 Qy 2326 gaaagtaac 2385
 Db 2451 GAAAGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2510
 Qy 2386 gtcatgtagcagcattgtgattacacacacacacacacacacacacacacacacacacac 2445
 Db 2511 GTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2570
 Qy 2446 tgggtgaac 2505
 Db 2571 TGGTATATGACATCTTGAAGAGGCTATGATGATGATGATGATGATGATGATGATGATG 2630
 Qy 2506 atgaattgaac 2539
 Db 2631 AAGCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2664
 RESULT 3
 PSSBEIGEN 3549 bp mRNA PLN 25-JUL-1995
 LOCUS P.sativum mRNA for starch branching enzyme I.
 DEFINITION X80009
 ACCESSION

VERSION X80009.1 GI:510545
 KEYWORDS SBEI gene; starch branching enzyme I.
 SOURCE pea
 ORGANISM Pisum sativum
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Pisum.
 1 (bases 1 to 3549)
 AUTHORS Burton,R.A., Bewley,J.D., Smith,A.M., Bhattacharyya,M.K., Tatge,H., Ring,S., Bull,V., Hamblin,W.D., and Martin,C.
 Starch branching enzymes belonging to distinct enzyme families are differentially expressed during pea embryo development
 JOURNAL MEDLINE
 Plant J. 7 (1), 3-15 (1995)
 REFERENCE 95201826
 2 (bases 1 to 3549)
 AUTHORS Burton,R.A.
 Direct Submission
 Submitted (01-JUL-1994) R.A. Burton, John Innes Institute, Colney Lane, Norwich NR4 7UH, UK
 JOURNAL
 TITLE
 FEATURES
 source
 1.3549
 /organism="Pisum sativum"
 /db_xref="taxon:3888"
 /dev_stage="embryo"
 /clone_lib="CDNA LAMBDA gt11"
 /cell_line="J1:430 Bcl19BR"
 /transcript_id="J1:430 Bcl19BR"
 /transcript_peptide 220..363
 /gene="SBEI"
 /gene_synonym="SBEI"
 /codon_start=1
 /product="starch branching enzyme I"
 /protein_id="CA56319.1"
 /db_xref="GI:1345570"
 /db_xref="SPTREMBL:Q41058"
 /translation="MAYTISGIREPVEVLSIKSLKCDLRASSHSFLKNNSSPSRTSLYAFSRSEKSTSLAESDKVLLPEQDMSVSLADLENDPITSEDAQMLELTKDGNKYNDISTSYREVDEKGSYSSLVYVNTDQTKRYSVSDKKVADKRPKIPPGTGOKIYEIDPLAORHOLDFEYGYKRLREIDYKREGGLAASGYSKRPRTSATGIVREMAPAKSAALVGPENNNPMDVNTDAFVWEFLPNNADSGPPPHGSRKITMDPSGKDSIPMKIFVOAPELIPNGITDPEEVEVHERHPQKPOSLRIYESHINSSPEKINTYANFROVDLPRIKLGNVAQVIAIOEHSYASFGYHTNFFAPSRREGTDEDLKSLIDRAHEGLVAMDIVSHSSNNLIDGIMFEDGTGDFHFPGRGYHMMWDSLEFNYGMEVLYRLSNARWMLDEKDFGDFGVTSMMYTHGLQVSEPTGNYSEFGLATDVEAVYVMYVNDLHGLFPAVSLGSDVSGMPFCIPDDGGIGENYRLHAAVADKWEILKODEDMRMEDYIHTLNRWLEKCYVYASHSQALYGDKTLAEWLNKMDMTFALDRPSTPLDRGIALHKMRLITWLGJGEGITNEMNGEHP EMDIPRGEQHLPNKGLIVGNNNSYDKRRFEDGLADLYLRYHMQEFDRAHMLEERYGFMPSSEHOYISRKNEGDVLIIFERDNIYFVFNHMTYSYDYRVGCLPKRYLVDSDDLTGFGEFNRLNHTAEYFTSEGWDPRFSLVYAPSRVAVYALADGVSEPLEIS DQVESEPIELSGVSEPIELSYEABSEPIERSVESESETTQSVSESETTQSV EYESETNO"
 BASE COUNT 1061 a 672 c 760 g 1056 t
 ORIGIN
 gene
 mat_peptide
 /gene="SBEI"
 /gene_synonym="SBEI"
 /gene="SBEI"
 /gene_synonym="SBEI"
 Query Match 50.6%; Score 1475.2; DB 14; Length 3549;
 Best Local Similarity 80.7%; Pred. No. 0;
 Matches 1723; Conservative 0; Mismatches 413; Indels 0; Gaps 0;
 Qy 398 catcgaaaatgtgatctaaacacagtcattctccaccccgagagggcaagaat 457
 Db 663 CAAGAAAGTAAAGTAGATTAACCTTAAGATCAATTCACCCGGTACTGGGCAAAAT 722
 Qy 458 atagacatagatccaaggttagcaggttcgtaacacacatagatccggtattaca 517
 Db 723 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 782
 Qy 518 gtacaaaagactccgagaagaatgtacacagatgaagtagtctgtagatattctcgcg 577

QY 974 cgttggaatgagtagtaacgagccaggaatataacacatatgccaaactttagagatgagt 1033
 Db 541 TATTGGAATGAGTAGTCCGAGGAGCTTAATAATATATGACAGATTTAGAGATATGCT 600
 QY 1034 gcttcctgcacaaagcttgctacaaatgctgttcaatcctatggtcattcaagaaga 1093
 Db 601 ACTTCCGCTGATATAAAGAGCTTGCTACATATGCTCCAGATATATGCGCATTCAGAGCA 660
 QY 1094 ttcatatagtagtatttggtgtatcaatgcacaaactttatgagctagagccgatt 1153
 Db 661 TTCTTATATGAGTCAAGCTTGGCTATCATGTTAGCAATTTCTTGGACCAAGAGTGTGT 720
 QY 1154 tggagactcctgagattttaaagctcctaagataagaactcagagttggtcctctgt 1213
 Db 721 TGGGACTCCGAGATGATTTAATCTTGTGATGATAGACCCATGACCTTGAGCTGATGT 780
 QY 1214 tctatgataatgatttcaatgacatgacataactaaactagcttgatggctgataatgt 1273
 Db 781 TCTATGATGATATTTGTCACACTGCTATGCTGACACCGGGTTATCATTTGATGTGGA 840
 QY 1274 tgaatgagagatgagtaacactcctcctgacacagaggtgacatgattgagga 1333
 Db 841 TGATGAGTACAGATAGTTGTTATTTCCACTCTGGAACCGGGTTATCATTTGATGTGGA 900
 QY 1334 cttcgcctttcaactatgaggtggtggaagttcctaagttctcttcaaatgcaag 1393
 Db 901 TTTCTGCTCTTCACTACATGAGAACTGGGAGATGAGTATGCTGCTCAATATGCAAG 960
 QY 1394 gtgttggttgagtagtaacagtttgatggttcaagatttgatgggtgagttcaatgat 1453
 Db 961 ATGTGTTGTTGAGTATACAGTTTGAATGCTTCAATGATGATGATGATGATGATGAT 1020
 QY 1454 gtaacccaatgagatgagtagatgattacccggaactcaactgatacttgata 1513
 Db 1021 GTATATCTCATATGAGGTGAGTGAATGCTGAGAACTGAAATGATGATGATGATGAT 1080
 QY 1514 tgaactatgtagatgagtggtgttatttgatggtgtgtgtaagtatgatactgagct 1573
 Db 1081 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 QY 1574 cttcccaagaggtgacacatgagtagatgatttgatggttcaactgatacttgata 1633
 Db 1141 CTTCCTGAGGCAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 QY 1634 gattgaagtagtgggt 1693
 Db 1201 GGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1694 ggttgaatattcagaagaagagatgagtagtgaatggtgagtagtgaatgagtagt 1753
 Db 1261 GATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 QY 1754 gacacacaggggt 1813
 Db 1321 TACTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 QY 1814 ttttggtgacaaatattcatttgcattgtagtagtagtagtagtagtagtagtagtag 1873
 Db 1381 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1874 tcttgacagacacatcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1933
 Db 1441 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 QY 1934 gcttattacacagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 1993
 Db 1501 ACTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 QY 1994 aaccccccagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2053
 Db 1561 TCACCCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620

QY 2054 tccctgggaacattacagattatgataaataacgagcgttaggtttgacttagtagcaataa 2113
 Db 1621 CCTCGAACAATTTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 QY 2114 gacttgaatgataacatgagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2173
 Db 1681 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 QY 2174 ctatggttcatgacttctgagacacatcatalcacaagaagtagtagtagtagtagtagtagtag 2233
 Db 1741 ATAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 QY 2234 cattgtcttcgagagggggaacactggttttgattatcaatttcaattgtagtagtagtag 2293
 Db 1801 GATCATTTTGAAGGGGGTCACTGCTGTTGTTCTTCAATTTCCACTGACCAATATGTTA 1860
 QY 2294 ttcggaattccgaggt 2353
 Db 1861 TTGGAATACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 QY 2354 tgaacttcttgtagaggt 2413
 Db 1921 CACTCGCTGTTGAGGCTTGGCGAGTTTCAACCCGATGAGATTTTTCACATTCGA 1980
 QY 2414 aggtgtgtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2473
 Db 1981 AGGATACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 QY 2474 ggtctatgctttagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtagtag 2503
 Db 2041 GGATGAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2070

RESULT 6

ATU22428 2542 bp mRNA PLN 28-JUN-1996
 LOCUS Arabidopsis thaliana starch branching enzyme class II mRNA
 DEFINITION (sbe2-2), partial cds.
 ACCESSION U22428
 VERSION U22428.1 GI:726489
 KEYWORDS starch branching enzyme; starch; Arabidopsis.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2542)
 Fisher, D.K., Gao, M., Kim, K.N., Boyer, C.D. and Gullitman, M.J.
 Two closely related cDNAs encoding starch branching enzyme from
 Arabidopsis thaliana
 Plant Mol. Biol. 30 (1), 97-108 (1996)
 96197401

JOURNAL MEDLINE
 REFERENCE 2 (bases 1 to 2542)
 AUTHORS Fisher, D.K., Gao, M., Kim, K.N., Boyer, C.D. and Gullitman, M.J.
 TITLE Direct Submissions
 JOURNAL Submitted (09-MAR-1995) Dane K. Fisher, Horticulture, Pennsylvania
 State University, 103 Tyson Bldg., University Park, PA 16802, USA
 FEATURES
 source
 1. 2542
 /organism="Arabidopsis thaliana"
 /strain="ecotype Columbia"
 /db_xref="taxon:3702"
 /tissue_type="hypocotyl"
 1. 2403
 /gene="sbe2-2"
 <1. 2403
 /gene="sbe2-2"
 /RC_number="2.4.1.18"
 /codon_start=1
 /function="1,4-alpha-d-glucan:1,4-alpha-glucan
 6-alpha-d-(1,4-alpha-d-glucano)-transferase"
 /product="starch branching enzyme class II"
 /protein_id="AB03100.1"

gene
 CDS
 1. 2403
 /gene="sbe2-2"
 /RC_number="2.4.1.18"
 /codon_start=1
 /function="1,4-alpha-d-glucan:1,4-alpha-glucan
 6-alpha-d-(1,4-alpha-d-glucano)-transferase"
 /product="starch branching enzyme class II"
 /protein_id="AB03100.1"

QY	2102	AATTCATATTCACGAAAGAACGACACCATATGAGTAATCGTATTCGAAAGAGGATATCTCG	2161
Db	2102	AATTCATATTCACGAAAGAACGACACCATATGAGTAATCGTATTCGAAAGAGGATATCTCG	2161
QY	2260	tttttgatttcaatttcaattgagctagcagcagctattcggattaccagagttgctgctttaa	2319
Db	2162	TCCTTGTCTTTAACTTTACCTGTCACCTGACCGAGCTACTTGTATTAACCGCATGTGGTGC	2221
QY	2320	agccagcaagaatcacaaatagcttgcctgatttcagatcatatccttgtttgagcctttgca	2379
Db	2222	ACCCGAGCAAAATATATTAAGATCGTATGTGACCTCGGACGACATCCCTCTTGTGGTGAATCA	2281
QY	2380	ggcttagctagctagctagcagcagcactttagcctttgaaaggtgctgacatataccgctcat	2439
Db	2282	GGCTTCGAGCCGACGACGAGCTACTTCACTTATGATGGCTTATAGACGACGACGACGACG	2341
QY	2440	cccttcatgtgttatacccatgtagaagacagcagctgtctcatgctttagtggaagatga	2497
Db	2342	CCCTCATGAGTGCTATGACACCCCTGTAGAACCCGCGCTGGTTATGCTTTAGCAAAACGACGA	2399
RESULT	7		
STSEBII			
LOCUS	STSEBII	2493 bp	mRNA
DEFINITION	Solanum tuberosum mRNA for starch branching enzyme II.	PLN	27-MAY-1998
ACCESSION	AJ0000004		
VERSION	AJ0000004.1	GI:2764395	
KEYWORDS	Sde-II gene; starch branching enzyme II.		
SOURCE	Potato.		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
AUTHORS	Larsson,C.T.A.		
TITLE	Direct Submission		
REFERENCE	Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell Research, Genetic Center, Swedish University of Agricultural Sciences, Box 7055, S-750 07 Uppsala, SWEDEN		
AUTHORS	Larsson,C.T., Khoshnoodi,V., Ek,B., Rask,L. and Larsson,H.		
TITLE	Molecular cloning and characterization of starch-branching enzyme II from potato		
JOURNAL	Plant Mol. Biol. 37 (3), 505-511 (1998)		
MEDLINE	98278379		
FEATURES			
source	Location/Qualifiers		
	1..2493		
	/organism="Solanum tuberosum"		
	/plasmid="pALSB-II (#123)"		
	/coulivar="Amanda"		
	/db_xref="taxon:4113"		
	1..2490		
	/gene="Sbe-II"		
	/EC_number="2.4.1.18"		
	/function="branches 1,4-alpha glucans"		
	/product="SBE-II"		
	1..2493		
	/gene="Sbe-II"		
	/EC_number="2.4.1.18"		
	/function="branches 1,4-alpha glucans"		
	/codon_start=1		
	/product="starch branching enzyme II, SBE-II"		
	/protein_id="CAA03846.1"		
	/db_xref="GI:2764396"		
	/db_xref="SPRMBL:04953"		
	/translation="EKSSYNSRSRSTYAAAGKYIVETQSDSSSSSTQDEFETETSP ENSASINDUSQWMEHAISOIKTNDVRESSDUGSVEYEDFASLIQLOEGKLEKSK TLNISEETIITDESRIKREKGIPEPGLQKRIYEDPLTNRHLDVRSYKKLRRAI DKTBGGLEAVNSKRGKEMGKTSRATGITYRENAPOAQSALIGFNMDANADIMTNE GFWGEIYLPANNDVGSIPAIGHGSRVKTIRMDPTSGVADSIPAWINYSIQLPETIPYNGIY VQPEEERITFQHPRRKKKSLRIYESHIGSSSEPKINSYVNRDDEVLPRIKUGIY AVOALMOEHSYISAFGYHTNVEFAPSRSFGTPDDTLISIDKAHEIGIYVMDIYHSH ASNNITDGLNMFQGDSCYFHSAGANGHYMMMDSKLFTYGNWEVLTITLISNARKWIDDEF		
gene	mat_peptide		
CDS	2493		

Query Match	47.5%;	Score 1384.8;	DB 15;	Length 2493;
Best Local Similarity	76.8%;	Pred. No. 0;		
Matches 1692;	Conservative	0;	Mismatches 512;	Indels 0;
			Gaps 0;	
347	lgttggaagtgaagtaataaagaatctgttccaatgcggagacagttagatcaga	445 c	595 g	711 t
285	tggtaaacctggagacgtctttaaacaattttaaactcttgaaagacaattat			
407	aattgatactaaaccaaaggtccatctccaccggagaggaagaataatgat			
345	tgatagatcagagagagagggcattccctccacttgatggaattatggaat			
467	agatccaagcttgacaagctcttcgtcaaacaccatagattaccggtatcca			
405	agaccccccttttgacaaactatctgccaacaccttgattacaggtatcca			
527	accctgagagaagaattgacaagtatagaagtgatctgtgatcatcttcgt			
465	actgagagagagcaattgacaaatgaaaggggtttggaaaccttttctgtg			
587	aaagtgtgttcttcacagcagtgaacaggaataactatagagatgggcaca			
525	aaaaatgggtttcacctcgatgctacacagatattaccttgatagggcctc			
647	tacgtggtcgtcatgtgatctggagattccaatactggaatccctaagtgc			
585	ccagtcagctgcccctcattggagagattccaaatmtggagacaaattctg			
707	tcagaatgagtggtgtctgtagagatcttttcgcgaataatgagatgttcc			
645	tgcgaatgaatttggtgctcgtggagattttctcccaaaatggatggtcttc			
767	aattcccatggtctcgaagtaagaatacgaatgatactccatctgccaaca			
705	aatttcctatgggtccacagtgaaatgaaatgacacatccatcaggttaag			
827	tattctcgtcgttgatcaagttctcagtccaagcaacaggtgaactccata			
765	catctctcgttgatcaactctcttttacacgtctccgatgaattccatata			
887	atactatgatactcccgagagagaagatagtgttcaaaaatccctcagcca			
825	atattatgattcaccgccgaagagagagatgattttccaaacaccacgcca			
947	aaaataccttcgagttatgatgctgcgcgtttgataatgataagagcaata			
885	aaagtcgttgagatattatgaaatctcattatgaaatgagatgcccgaact			
1007	caaatatccaaacttagagatgatagtgtctctgcgcgcataaaaagcttg			
945	ctcatagctggaattttgagatgaaatgattcttcccatataaaaacttgg			
1067	tgttcagctcatggtcattccaagaatcatalatagttagtttgggtacag			
1005	gggtcaaatattatgctctatccaagacattctttatgacagttttggtat			
1127	aaactttatgagcagcagcgagatttggactcctgtgtattcaagttctaa			
1065	aaatttttttgcacacagacccggttttgaaactcccgacgaccttaagt			
1187	taaaagctcagagttagttcttcttctcagatattgtcttacaagatcag			

